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(54) Title: IMPROVED BACILLUS HOST CELL

(57) Abstract: A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 191, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions

Improved Bacillus Host Cell

TECHNICAL FIELD

Bacillus sp. are attractive hosts for the production of heterologous proteins due their ability to secrete proteins directly into the culture medium. They have a high capacity for protein secretion, are genetically highly amenable, nonpathogenic and free of endotoxins, and consequently a large variety of proteins from different organisms have been efficiently produced and secreted in *Bacillus sp. i.e.* in *Bacillus licheniformis.*

In the highly competitive biotech industry, even slightly improved *Bacillus* host cells are in demand, which may provide more attractive production systems, or may even just be alternative production systems.

BACKGROUND

Many industrial products of commercial interest can be produced biologically in *Bacillus sp.* host cells e.g. heterologous polypeptides, amino acids, carbohydrates etc. Some of these products are sold as process aids, intermediates, or even end-products in the food and feed industries as well as in the pharmaceutical industry. There are increasingly strict regulations that must be complied with when producing such products in microbial production hosts for sale in these industries, for instance the presence of bacterial spores in the products is seen as a problem. When producing in *Bacillus licheniformis* it is thus desirable to ensure that the host cell is not capable of forming spores.

SUMMARY

A problem to be solved by the present invention is how to obtain a *Bacillus licheniformis* host cell incapable of forming spores, or how to impair the sporulation process of said cell. The present invention provides a solution to the problem by providing a *Bacillus licheniformis* host cell which has a reduced capacity to produce one or more polypeptide(s) involved in sporulation.

Accordingly, in a first aspect the invention relates to a *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129 (both included), or in SEQ ID NO's: 2 to 191 (both included), preferably at least 85% identical, more preferably at least 90% identical, still more preferably at least 95% identical, and most preferably at least 97% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129 (both included), or in SEQ ID NO's: 2 to 191 (both included), wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than

the parent host cell, when they are cultivated under comparable conditions. Preferably the mutant host cell expresses at least 10% less, more preferably at least 20% less, still more preferably at least 30% less, even more preferably at least 40% less, yet more preferably at least 50% less, or at least 60% less, or at least 70% less, or at least 80%, or most preferably at least 90% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions. Most preferably the mutant host cell expresses absolutely nothing of the one or more polypeptide(s) involved in sporulation.

Comparable conditions of cultivation must be used in order to compare the expression level of the one or more polypeptide(s) involved in sporulation in a mutant host cell of the invention with that in a parent host cell. They are cultivated separately under identical conditions in identical setups, of course allowing for the usual standard deviations of the operating parameters normally associated with growth experiments, such as temperature control etc. The quantification of the expression level of the one or more polypeptide(s) is done by standard text-book assay techniques as known in the art e.g. mRNA quantification or immuno-based assays.

In a second aspect the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the previous aspect in a suitable medium, whereby the said product is produced.

Finally, an aspect of the invention relates to a use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

DEFINITIONS

Nucleic acid construct: When used herein, the term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

Control sequence: The term "control sequences" is defined herein to include all components, which are necessary or advantageous for the expression of a polypeptide of the present

invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleotide sequence encoding a polypeptide.

Operably linked: The term “operably linked” is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the expression of a polypeptide.

Coding sequence: When used herein the term “coding sequence” is intended to cover a nucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA, cDNA, and recombinant nucleotide sequences.

Expression: In the present context, the term “expression” includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

Expression vector: In the present context, the term “expression vector” covers a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of the invention, and which is operably linked to additional segments that provide for its transcription.

DETAILED DISCLOSURE

A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 191 (both included), wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.

The term "parent host cell" in the context of the present invention means a cell which is genetically identical, or isogenic, to the progeny mutant or mutant cell of the present

invention, except for the mutated one or more gene(s) encoding one or more polypeptide(s) involved in sporulation in said mutant.

The degree of identity, or %-identity of polypeptide sequences can suitably be investigated by aligning the sequences using a computer program known in the art, such as "GAP" provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711)(Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453). Using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3".

An object of the present invention is to provide a culture medium free of bacterial spores so as to reduce the product purification to a minimum, and to comply with regulatory requirements. This may be done according to the invention by reducing or even completely abolishing the expression of one or more gene(s) encoding a native polypeptide(s) involved in sporulation via mutagenisation of that (those) gene(s). One of the very well-known method of ensuring that a gene is not expressed into an active polypeptide within a cell is simply to delete or partially delete the encoding gene. Many techniques have been described in the art on how to specifically delete or partially delete one or more gene(s) in the genome of a cell, and certainly from the genome of a *Bacillus licheniformis* cell (see e.g. Novozymes A/S WO 01/90393, Novozymes A/S WO 02/00907). Accordingly, a preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more polypeptide(s) involved in sporulation.

A preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated in two or more genes encoding two or more polypeptides involved in sporulation.

The product of interest to be produced by the mutant host cell of the first aspect may be one or more polypeptide(s) encoded by one or more heterologous gene(s). Consequently, a preferred embodiment of the present invention relates to a host cell of the first aspect, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

In the industrial production of polypeptides it is of interest to achieve a product yield as high as possible. One way to increase the yield is to increase the copy number of a gene

encoding a polypeptide of interest. This can be done by placing the gene on a high copy number plasmid. However, plasmids are unstable and are often lost from the host cells if there is no selective pressure during the cultivation of the host cells. Another way to increase the copy number of the gene of interest is to integrate it into the host cell chromosome in multiple copies. Integration of two genes has been described in WO 91/09129 and WO 94/14968 (Novozymes A/S) the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) is present in at least two copies, preferably at least 4 copies, and most preferably at least 6 copies. In another embodiment the heterologous gene(s) is present in at least ten copies. If carried on a plasmid the gene(s) may be present in several hundred copies per cell, so in a still further embodiment of the present invention the heterologous gene(s) is present in at least 100 copies.

Integration of two genes closely spaced in anti-parallel tandem to achieve better stability has been described in WO 99/41358 (Novozymes A/S) the content of which is hereby incorporated by reference, as well as the stable chromosomal multi-copy integration of genes described in WO 02/00907 (Novozymes A/S) the content of which is incorporated herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

Selection of chromosomal integrant has for convenience resulted in the use of selectable markers such as antibiotic resistance markers. However it is desirable if possible to avoid the use of antibiotic marker genes. WO 01/90393 discloses a method for the integration of a gene in the chromosome of a host cell without leaving antibiotic resistance markers behind in the strain, the content of which is hereby incorporated by reference A preferred embodiment of the present invention relates to a host cell of the first aspect wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker gene(s) at the site of integration.

The present invention also relates to nucleic acid constructs comprising a nucleotide sequence encoding a product of interest, which may be operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

A nucleotide sequence encoding a polypeptide ofinterest may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the nucleotide sequence prior to its insertion into a vector may be desirable or necessary depending on the expression

vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

Other ways of increasing the product yield would be to increase promoter activity of the specific promoter regulating the expression of a specific gene of interest. Also a more general increase in the activity of several promoters at the same time could lead to an improved product yield. The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the E. coli lac operon, Streptomyces coelicolor agarase gene (dagA), Bacillus subtilis levansucrase gene (sacB), Bacillus licheniformis alpha-amylase gene (amyL), Bacillus stearothermophilus maltogenic amylase gene (amyM), Bacillus amyloliquefaciens alpha-amylase gene (amyQ), Bacillus licheniformis penicillinase gene (penP), Bacillus subtilis xylA and xylB genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, Proceedings of the National Academy of Sciences USA 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, Proceedings of the National Academy of Sciences USA 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242: 74-94; and in Sambrook et al., 1989, supra.

Other useful promoters are described in WO 93/10249, WO 98/07846, and WO 99/43835 (Novozymes A/S) the contents of which are incorporated fully herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for Bacillus NCIB 11837 maltogenic amylase, Bacillus stearothermophilus alpha-amylase, Bacillus licheniformis subtilisin, Bacillus licheniformis beta-lactamase, Bacillus stearothermophilus neutral proteases (nprT, nprS, nprM), and Bacillus subtilis prsA. Further signal peptides are described by Simonen and Palva, 1993, Microbiological Reviews 57: 109-137.

The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding

region may be obtained from the genes for Bacillus subtilis alkaline protease (aprE), Bacillus subtilis neutral protease (nprT), Saccharomyces cerevisiae alpha-factor, Rhizomucor miehei aspartic proteinase, and Myceliophthora thermophila laccase (WO 95/33836).

Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.

The present invention also relates to recombinant expression vectors comprising the nucleic acid construct of the invention. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleotide sequence encoding the polypeptide at such sites. Alternatively, the nucleotide sequence of the present invention may be expressed by inserting the nucleotide sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication,

e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

Examples of bacterial selectable markers are the dal genes from Bacillus subtilis or Bacillus licheniformis, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance.

The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in E. coli, and pUB110, pE194, pTA1060, and pAMß1 permitting replication in Bacillus. The origin of replication may be one having a mutation which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proceedings of the National Academy of Sciences USA 75: 1433).

More than one copy of a nucleotide sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, supra).

The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, Molecular General Genetics 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, Journal of Bacteriology 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, Journal of Molecular Biology 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, Biotechniques 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, Journal of Bacteriology 169: 5771-5278).

A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon. The term "operon" in the context of the present invention means a polynucleotide comprising several genes that are clustered and perhaps even transcribed together into a polycistronic mRNA, e.g. genes coding for the enzymes of a metabolic pathway. The transcription of an operon may be initiated at a promoter region and controlled by a neighboring regulatory gene, which encodes a regulatory protein, which in turn binds to the operator sequence in the operon to respectively inhibit or enhance the transcription. The

gene or the operon can be carried on a suitable plasmid that can be stably maintained, e.g. capable of stable autonomous replication in the host cell (the choice of plasmid will typically depend on the compatibility of the plasmid with the host cell into which the plasmid is to be introduced) or it can be carried on the chromosome of the host. The said gene may be endogenous to the host cell in which case the product of interest is a protein naturally produced by the host cell and in most cases the gene will be in it normal position on the chromosome. If the gene encoding the product of interest is an exogenous gene, the gene could either be carried on a suitable plasmid or it could be integrated on the host chromosome. In one embodiment of the invention the eubacterium is a recombinant eubacterium. Also the product of interest may in another embodiment be a recombinant protein.

The product of interest is any gene product or product of a metabolic pathway which is industrially useful and which can be produced in a bacterial cell such as a *B. licheniformis.*

In one preferred embodiment, the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

In another preferred embodiment, the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

Yet another embodiment relates to a host cell of the first aspect, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants, and preferably the carbohydrates comprise hyaluronic acid.

In one embodiment the heterologous polypeptide(s) is an enzyme, particularly the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). Preferably the enzyme is an enzyme with an activity selected from the group consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase. Preferably the enzyme is an amylase or a mannanase.

A second aspect of the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the first aspect of the invention in a suitable medium, whereby the said product is produced. One embodiment relates to a process of the second aspect, further comprising isolating or purifying the product of interest. Suitable media for the cultivation is described below as well as methods for the purification or isolation of the produced product which is an optional additional step to the process of the present invention.

In the production methods of the present invention, the cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

The medium used to culture the cells may be any conventional medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection). The media are prepared using procedures known in the art (see, *e.g.*, references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, *More Gene Manipulations in Fungi*, Academic Press, CA, 1991).

The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide as described herein.

The resulting polypeptide may be recovered by methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures

including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

The polypeptides of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (*e.g.*, ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (*e.g.*, preparative isoelectric focusing), differential solubility (*e.g.*, ammonium sulfate precipitation), SDS-PAGE, or extraction (see, *e.g.*, *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

A third aspect of the present invention relates to the use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced, and optionally isolating or purifying the produced product.

CLAIMS

1. A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 191, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.

2. The host cell according to claim 1, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more polypeptide(s) involved in sporulation.

3. The host cell according to any of claims 1 – 2, which is mutated in two or more genes encoding two or more polypeptides involved in sporulation.

4. The host cell according to any of claims 1 – 3, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

5. The host cell according to claim 4, wherein the heterologous gene(s) is present in at least two copies.

6. The host cell according to claim 4 or 5, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

7. The host cell according to any of claims 4 - 6, wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes at the site of integration.

8. The host cell according to any of claims 4 - 7, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

9. The host cell according to any of claims 4 – 8, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon.

10. The host cell according to any of claims 4 – 9, wherein the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

11. The host cell according to any of claims 4 – 9, wherein the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

12. The host cell according to claim 11, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants.

13. The host cell according to claim 12, wherein the carbohydrates comprise hyaluronic acid.

14. The host cell according to any of claims 4 – 9, wherein the heterologous polypeptide(s) is an enzyme, preferably a secreted enzyme.

15. The host cell according to claim 14, wherein the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6).

16. The host cell according to claim 15, wherein the enzyme is an enzyme with an activity selected from the group of enzyme activities consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, and xylanase.

17. The host cell according to claim 16, wherein the enzyme is an amylase or a mannanase.

18. A process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in any of the claims 1 - 17 in a suitable medium, whereby the said product is produced.

19. The process according to claim 18, further comprising isolating or purifying the product of interest.

20. A use of a *Bacillus licheniformis* mutant host cell as defined in any of the claims 1 - 17 for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

21. The use according to claim 20 further comprising isolating or purifying the product of interest.

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       Jørgensen, Steen Troels
       Olesen, Peter Bjarke
       Andersen, Jens Tønne
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<120>  Improved Bacillus Host Cell

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acgagcaggg acggaggatc aagcgaaaga attccgatgt gcggggttcc ttatcattcc 1366

tgctcttcgt atatcgaaca gctcattaaa aaaggctata aagtcgcgat ctgtgaacag 1426

gtggaggacc ctaaatcggc caaaggagtc gtcaaaaggg aagtcgtgca gctgatcaca 1486

cccggcaccg tgatggacgg caaagggatt catgaaaatg aaaacaactt tatcgcctct 1546

gtc 1549

<210> 8
<211> 182
<212> PRT
<213> Bacillus licheniformis

<400> 8

Met Ser Glu Tyr Arg Glu Ile Ile Thr Lys Ala Val Val Ala Lys Gly
1 5 10 15

Arg Lys Phe Thr Gln Ser Thr His Thr Ile Ser Pro Ser Gln Lys Pro
20 25 30

Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His Lys Tyr Asp Ala Glu
35 40 45

Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr Tyr Asp Ile Asn Val
50 55 60

Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu Val Val Thr Glu Arg
65 70 75 80

Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr Arg Asp Lys Asn Tyr
85 90 95

Leu Asp Asp Glu His Glu Val Ile Ala Lys Val Leu Gln Gln Pro Asn
100 105 110

Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn Lys Val Val Val Gln
115 120 125

Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly Glu Thr Lys Val Val
130 135 140

Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp Glu Glu Glu Ala Trp
145 150 155 160

Glu Glu Glu Leu Asp Glu Glu Leu Glu Asp Ile Asn Pro Glu Phe Leu
165 170 175

Val Gly Asp Pro Glu Glu
180

<210> 9
<211> 1477
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(974)

<400> 9
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gcaatttcat tttcaaataa agacgatgag atgagcaggt ctcggccttc tctcattgtt 120

tctttattct aacataaggt caaatcgcaa gtaaaacgat cataaggctt gaaagcgagc 180

gaatgttcca tgtgaaacag tgtcagtcga gaaaccccga tttttcttta tttttctttc 240

tcgcctttct gatcagcaac aatataatca aaactgcgac cagaagcgtc acgcgaagcc 300

ctccgctcaa aaatagaaaa aagtccttca acatatccaa cacattgatc acctctcact 360

gttgtcactt agatgcaaaa atcccgtatt atttgacttc ccctttccaa aacggtctaa 420

aacgtccctc agattcttct taacctttag acggtaatgg gcatatgctg actaagaaaa 480

agcaataaag gagaatatga atg aca aca aaa aca ttg gct tgg cat gaa acg 533
Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr
1 5 10

ttg gag ttg cat gaa cta atc gcg gca cag tct gtc gga ttg gtg aag 581
Leu Glu Leu His Glu Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys
15 20 25

atc aag aaa agc atg aag aaa atc agc gac cct cag tta aga cag ctt 629
Ile Lys Lys Ser Met Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu
30 35 40

tac agc gtg tca gca aaa gca ttg gag caa aat tta aga gag ctt ctt 677
Tyr Ser Val Ser Ala Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu
45 50 55

ccc ttt ttg cca aaa gct cca gca ttt cag cgg gag gat gaa cgg gct 725
Pro Phe Leu Pro Lys Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala
60 65 70 75

gac ttg tat ttt gat gcg ggt gat ctg ttg gtg ctg gcg aaa acg acc 773
Asp Leu Tyr Phe Asp Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr
80 85 90

gtt cga aac tat gcg att gcg atc acg gaa acg gcg acg ccc gag ctc 821
Val Arg Asn Tyr Ala Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu
95 100 105

agg aga gtg ctt gtt aaa caa atc aat gcg gcc att aag ttg cat gaa 869
Arg Arg Val Leu Val Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu
110 115 120

caa gtt ttt tat ttt atg tac caa aga ggc tta tat ccc gcc tat aac 917

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Gln Val Phe Tyr Phe Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn
    125                 130                 135

ctc gtc gac ctg cta aaa ggc gac gcc atg cat gcg caa aaa gcg ata     965
Leu Val Asp Leu Leu Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile
140                 145                 150                 155

tcg atg aga taaaaaagcc agcgaggata gaatcctcac tggctctgtt            1014
Ser Met Arg

ttttgctatt ttacgattaa aaccggacac ttcactcttt tcgccacttt atggctgaca  1074

cttccgagca ccatttcctg caaagtgttc agcccctgc ttccgataat cacgatatca   1134

acatcatgat ggttggcgta cgatacaatg gccgggcccg gatccccgtg ctgcatcgtc  1194

atttgatagg gaacggccgc ctgttttaat ttattttcta tcgacagcag cctgctgcgc  1254

cgttcgcgtt cgagttctgt acggttttcg ctatgcagga cttcatgttt tgctctcgca  1314

taatccaata cataaatcat gtcgacgacc gcttcgtttg acatggaagc cagatgaatc  1374

gcatgatcgg cagctctttc agaatgcttg gaaccgtcag cagccagcag tatatgtcta  1434

tacacccttc atcacccgtt tcttagtgat ttgacactga acg                    1477


<210>  10
<211>  158
<212>  PRT
<213>  Bacillus licheniformis

<400>  10

Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr Leu Glu Leu His Glu
1               5                   10                  15

Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys Ile Lys Lys Ser Met
            20                  25                  30

Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu Tyr Ser Val Ser Ala
        35                  40                  45

Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu Pro Phe Leu Pro Lys
    50                  55                  60

Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala Asp Leu Tyr Phe Asp
65                  70                  75                  80

Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr Val Arg Asn Tyr Ala
                85                  90                  95

Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu Arg Arg Val Leu Val
            100                 105                 110

Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu Gln Val Phe Tyr Phe
        115                 120                 125

Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn Leu Val Asp Leu Leu
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130 135 140

Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile Ser Met Arg
145 150 155

<210> 11
<211> 1752
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (183)..(1256)

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acatacgcgc cgtaaagaca agtgtactga ggcaaatgac tgtttttgtt caaacttagg 120

cggtctgctt ccgggacagg tttttttcac atatgatatg tcagctgaaa aaggaggaaa 180

tg atg atg agt gcc act gcc ttg ccg gcc ttt agg ctg cac att cat 227
Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His
1 5 10 15

ccg aag cat ctg ctt gag ttg aaa aaa gac gtc tgg agt gat gaa gcc 275
Pro Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala
20 25 30

gtt ccc ggc atg ctc ttg acc ggt tca gca aag acg cct gtc gca gtg 323
Val Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val
35 40 45

tca tac aga ggg gcc cac acc cgc aaa ctg acg aaa aaa tcc tat ttc 371
Ser Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe
50 55 60

att caa tat ccg gac aat aaa gaa aag gct gcg ttt cat ttg aac gcg 419
Ile Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala
65 70 75

gaa tat cat gat ccg tct ttc atc aga aac agg ctt tcc ttt cat ttt 467
Glu Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe
80 85 90 95

ttt gaa caa atc ggc gtc ctt gcg cca gca gca tca cac gtt ttc ctt 515
Phe Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu
100 105 110

tat atc aat gaa aaa aaa gaa ggc atc tat tta aaa atc gaa tct gtt 563
Tyr Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val
115 120 125

gac gat cat ttc tta aag agg aga aat tta gaa agg ggg gcc att tat 611
Asp Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr
130 135 140

tat gcc gtt gat gac gat gct aat ttt tct ctg ctg agt tcc ttc aat 659
Tyr Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn
145 150 155

aaa aag gct aag caa aat ctc atg cag gga tac gaa aga aaa acg ggt 707
Lys Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly
160 165 170 175

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tca agc cgc cac gat gac tac ctc cat gag ttt atc tac ttt atc aat      755
Ser Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn
                180                 185                 190

acc gcc aaa gac gac ata ttt gaa aaa gaa atc aaa cgc tat ctc gat      803
Thr Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp
            195                 200                 205

gtc aaa caa tat ttg ctg tgg ctc atc ggc gcc gtc tgc acc caa aat      851
Val Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn
        210                 215                 220

ttc gac ggc ttt gtc cat aat tac gcg ctt tat tta aac ggt cgc aca      899
Phe Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr
    225                 230                 235

aaa acg ttt caa atc att cca tgg gat tat gac gcg aca tgg gga cgg      947
Lys Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg
240                 245                 250                 255

aat att cac ggg gaa gaa atg gag cac aac cgg att ccg gcg aaa ggc      995
Asn Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly
                260                 265                 270

tat aat acg ctg tct gca agg ctg ctc gac atc ccg gct ttt caa tcc     1043
Tyr Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser
            275                 280                 285

caa tac ttt aat tta atg aaa aat gtc ttg cac cgc caa ttt aca atc     1091
Gln Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile
        290                 295                 300

agc cgg ctt tcg cgg tat gcg gta aac tgg cac gag aca atc gcg cct     1139
Ser Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro
    305                 310                 315

ttt ctt gaa cat gat cct tat aca acc gtc aca tac agc cgg ctc gaa     1187
Phe Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu
320                 325                 330                 335

gat gag caa aaa caa att ttt cat ttc atc gat cag agg aag cgg ttc     1235
Asp Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe
                340                 345                 350

ctg ctt ttc gag ctt tcc cga taatagactg tcgctgtcct ccgaaaaaaa        1286
Leu Leu Phe Glu Leu Ser Arg
            355

tgtcacattt tttgtcatat tggcgaaaaa aatccctttt acacaaaata aggtatacta   1346

gcaatatcaa ggacatcaat gcgctgaata cctgaaatta ccgactcaaa atacaaatcg   1406

aaagttggag actgccatga tgaacaataa aattgaagca aaaagactgg ccttatttga   1466

agctgccgaa aagttcggca tcaactccaa agaggccatt cgatgcagtc aggaattgga   1526

caacttgctg aatcaaagaa tgcaaaagga tgataactgc gtgcatgcgg aagaaagaaa   1586

aggccgccac acgtcatgac ctccgactgc aagctgcgcc tgatgccggc ctccttcctc   1646

ctccatttca tcatccgttg atttcgggtc gcagcttggg ctattcggcc attgtttttt   1706

gaacataaat catcgtgcaa ataccgtagg caagaatggc tgaagg                  1752

<210>  12
<211>  358
<212>  PRT
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<213> Bacillus licheniformis

<400> 12

Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His Pro
1 5 10 15

Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala Val
20 25 30

Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val Ser
35 40 45

Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe Ile
50 55 60

Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala Glu
65 70 75 80

Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe Phe
85 90 95

Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu Tyr
100 105 110

Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val Asp
115 120 125

Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr Tyr
130 135 140

Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn Lys
145 150 155 160

Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly Ser
165 170 175

Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn Thr
180 185 190

Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp Val
195 200 205

Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn Phe
210 215 220

Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr Lys
225 230 235 240

Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg Asn
245 250 255

Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly Tyr
260 265 270

Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser Gln
275 280 285

Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile Ser
290 295 300

Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro Phe
305 310 315 320

Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu Asp
325 330 335

Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe Leu
340 345 350

Leu Phe Glu Leu Ser Arg
355

<210> 13
<211> 1570
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1067)

<400> 13
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aaaagatact acagaacccc tccaaatcta tatctaggtt ttcagccccg cggccttccg 120

cagttttccc cgatggaggc gctgcaaaaa gggacgcttt ggcccgtatt ttacgatcat 180

tatgaaaatc cgtatgaaga tgggaggtaa ggagggtgac gaactcttta ccgcaagact 240

attataaaag gcttcatgaa attcaggctg ttgattttgt catcgttgag ctgatgctat 300

accttgacac acatcccgat gataccgatg ccatcaaaca atacaaccag tatgccggat 360

tttccagaaa actgaaagcg aagtttgaat caaaatacgg ccctttgatt caaggaagcc 420

cggatcagac ggaatcctat tggagctgga aaagaagtcc ttggccatgg caagtttaat 480

agaggaaggg agtcaggttc atg tgg ctt tat gag aaa aaa ctg cag tat cct 533
Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro
1 5 10

gtt agg gtg aga gaa tgc aat ccg aga ctt gcc aaa ttt ttg att gag 581
Val Arg Val Arg Glu Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu
15 20 25

caa tac ggc gga gcg gac ggc gaa ttg gct gcg gcg ctt cgc tat ttg 629
Gln Tyr Gly Gly Ala Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu
30 35 40

aac cag cgc tac agc ata ccc gat aaa gtc gtc gga ctg ctg acg gac 677

Asn Gln Arg Tyr Ser Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp
45 50 55

atc ggt acg gaa gag ttt gct cac ctt gaa atg att gcc acg atg gta 725
Ile Gly Thr Glu Glu Phe Ala His Leu Glu Met Ile Ala Thr Met Val
60 65 70 75

tat aaa tta aca aaa gac gcg acg ccc gag cag atg aag gaa gcc ggg 773
Tyr Lys Leu Thr Lys Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly
80 85 90

ctc ggc gat cat tac gca gac cat gac aaa gcc ctg ttt tat cat aac 821
Leu Gly Asp His Tyr Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn
95 100 105

gct gcc ggc gtt ccg ttc acc gct aca tac atc cag gca aaa ggc gat 869
Ala Ala Gly Val Pro Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp
110 115 120

ccg att gcc gat tta tat gaa gat ata gcg gct gaa gaa aaa gcg agg 917
Pro Ile Ala Asp Leu Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg
125 130 135

gct acg tat caa tgg ctg att gac atg tcg gat gat ccg gat tta aat 965
Ala Thr Tyr Gln Trp Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn
140 145 150 155

gac ggg ctg gcg ttt tta cgg gaa agg gaa atc gtt cat tca cag cgc 1013
Asp Gly Leu Ala Phe Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg
160 165 170

ttc cgc gaa gct gtc gaa att ttg aag gaa gag cgc gac cgt aaa aaa 1061
Phe Arg Glu Ala Val Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys
175 180 185

gtg ttt taaacagcaa aaagccgaaa atacgaccgt attttcggct ttttatttac 1117
Val Phe

tgcaccgggc tcgcaagcag ttctgctgcg cggtcgcgca gcacatattt ttgaactttt 1177

ccggatgcgg tcagcgggta ttcgtcgatc agaaatacgt actccggaat tttataatac 1237

gaaagctgtc ctttgcaaaa atctctgacg tcttcgagcg tcagcttttt gcccggcctg 1297

catttaataa aggcagccgt tttttccccg tacttttcat ccggaacgcc gacaacctgt 1357

acatcgacaa tatcctcatg ttcataaagg aattcctcta tttcacgcgg gtaaatgttt 1417

tccccgccgc ggacgatcat atcttttaag cgcccggtaa tcctcacgta tccgtcccgg 1477

tccatttctg ccaaatctcc ggtatggagc cagccgtctt catcgatggc ctttttgtg 1537

gcttcatcca ttttatagta gcctttcatg acg 1570

<210> 14
<211> 189
<212> PRT
<213> Bacillus licheniformis

<400> 14

Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro Val Arg Val Arg Glu
1 5 10 15

Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu Gln Tyr Gly Gly Ala

20 25 30

Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu Asn Gln Arg Tyr Ser
35 40 45

Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp Ile Gly Thr Glu Glu
50 55 60

Phe Ala His Leu Glu Met Ile Ala Thr Met Val Tyr Lys Leu Thr Lys
65 70 75 80

Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly Leu Gly Asp His Tyr
85 90 95

Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn Ala Ala Gly Val Pro
100 105 110

Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp Pro Ile Ala Asp Leu
115 120 125

Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg Ala Thr Tyr Gln Trp
130 135 140

Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn Asp Gly Leu Ala Phe
145 150 155 160

Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg Phe Arg Glu Ala Val
165 170 175

Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys Val Phe
180 185

<210> 15
<211> 1241
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (519)..(1028)

<400> 15
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tgaaaaactt caagagaacg tagatccgat aatgaaatca gttgttaaaa atatcttgaa 120

aaatcgggga gtaaccagcg ataaagttcg gacgctctca gaagaagaaa aagaaaatat 180

tttcaatatg ctggaagatc taaaaaaaca aaccgatgct ttggttcaaa aacagaaaga 240

aaaagcagcc gcaccgaatg aaaaagggac aaagagagaa aagaacgctg atgcgtcatc 300

agaaaatggc gagagaccaa gaagaagaag aaacagaaca aatagactga gagaaaaact 360

tcgacaacgg agggagcaag aaaacacagc aacagcggaa aattcaaccg agtcagatac 420

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ttcagcagaa aaaaatgggg atttgtagta gggtatctgt cttatacaag ttaaggagtt      480

acaacattta ataatagtaa atggaaggag gaaaagaa atg gaa aca aga cca tat      536
                                          Met Glu Thr Arg Pro Tyr
                                          1               5

tca tgg att gcg ctt gac ccg gaa tgc gaa cat cca ggc aac gat tat        584
Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu His Pro Gly Asn Asp Tyr
            10                  15                  20

cac cct agt tat cct aag aaa aaa tta tgt gac gac tat act tgc aac        632
His Pro Ser Tyr Pro Lys Lys Lys Leu Cys Asp Asp Tyr Thr Cys Asn
        25                  30                  35

tgt ggt agg aaa ggg caa aat ggc ttt atc gat tct gac cta gat caa        680
Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile Asp Ser Asp Leu Asp Gln
    40                  45                  50

ctt cat ctt aac aaa cag ctc tca gat gaa acg atc atc att aaa gac        728
Leu His Leu Asn Lys Gln Leu Ser Asp Glu Thr Ile Ile Ile Lys Asp
55                  60                  65                  70

tct tgt gat gtt caa gtc tca act gaa gac aca caa acg ttg gca tca        776
Ser Cys Asp Val Gln Val Ser Thr Glu Asp Thr Gln Thr Leu Ala Ser
                75                  80                  85

gtc atg aca gct gca caa aca cta gct gtt act att att ctc gcc att        824
Val Met Thr Ala Ala Gln Thr Leu Ala Val Thr Ile Ile Leu Ala Ile
            90                  95                  100

atc gat gat cct gat cta gcc gaa ctt gtc aca act gat ctg ttg cag        872
Ile Asp Asp Pro Asp Leu Ala Glu Leu Val Thr Thr Asp Leu Leu Gln
        105                 110                 115

gta act gcc aat aaa caa acg aac aga caa aaa ttg gtg atc gat aat        920
Val Thr Ala Asn Lys Gln Thr Asn Arg Gln Lys Leu Val Ile Asp Asn
    120                 125                 130

tcc aga aat gta cat gtc aca acc gaa gat aca gac aca gct atc atc        968
Ser Arg Asn Val His Val Thr Thr Glu Asp Thr Asp Thr Ala Ile Ile
135                 140                 145                 150

gta agc aca ttt gtt caa act gtt gta atc acc atc acc gcc ctt atc       1016
Val Ser Thr Phe Val Gln Thr Val Val Ile Thr Ile Thr Ala Leu Ile
                155                 160                 165

gtc ggc ctt cta taattcaaaa agcagagcca accagctctg cttttcttca           1068
Val Gly Leu Leu
            170

tttttataga cgattaccca caccaacaag ggcacgggta catatgttgt taaagactaa     1128

agtcaaatat ccctataaaa aggagctgaa atccatgagc tgcggaaaac accatggccg     1188

gcatgaaaat tgtgtatgcg atgcagtaga acagattata aaagaacagg atg            1241
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<210> 16
<211> 170
<212> PRT
<213> Bacillus licheniformis

<400> 16

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Met Glu Thr Arg Pro Tyr Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu
1               5                   10                  15
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His Pro Gly Asn Asp Tyr His Pro Ser Tyr Pro Lys Lys Lys Leu Cys
20 25 30

Asp Asp Tyr Thr Cys Asn Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile
35 40 45

Asp Ser Asp Leu Asp Gln Leu His Leu Asn Lys Gln Leu Ser Asp Glu
50 55 60

Thr Ile Ile Ile Lys Asp Ser Cys Asp Val Gln Val Ser Thr Glu Asp
65 70 75 80

Thr Gln Thr Leu Ala Ser Val Met Thr Ala Ala Gln Thr Leu Ala Val
85 90 95

Thr Ile Ile Leu Ala Ile Ile Asp Asp Pro Asp Leu Ala Glu Leu Val
100 105 110

Thr Thr Asp Leu Leu Gln Val Thr Ala Asn Lys Gln Thr Asn Arg Gln
115 120 125

Lys Leu Val Ile Asp Asn Ser Arg Asn Val His Val Thr Thr Glu Asp
130 135 140

Thr Asp Thr Ala Ile Ile Val Ser Thr Phe Val Gln Thr Val Val Ile
145 150 155 160

Thr Ile Thr Ala Leu Ile Val Gly Leu Leu
165 170

<210> 17
<211> 1516
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1013)

<400> 17
acgtcggtca cgccggggac cctaatatgg cacacggcaa agaagatgac tgcgggtgcg 60

ggccgggcca attcccggga ggttttccag gtgcggcgcc atatggacag atgccgcaaa 120

tgggagctcc gtacggtatg gggggatacg gacagcagcc tgcagggggga cagatgttta 180

acagaccgga agatgatgaa gactgattcg gaatgggacg atgatctatc gttccttttt 240

tattgtggac cgctataaac attttcatgc tatttaacgg gaatgtctat aactgtcaag 300

ggtaactctt cgcatcccgc acatcctaaa aaagagcgca atgctcaaat tcagcggttt 360

tcacgggggg tactaccatt ggacagcaag ctgaaagtgt tttcggggat tttgcttttg 420

acagcaggtc tatctgcatg cggaacgaac gacgctatag ataatggaaa caatacgcgc 480

ccgatcggat attatctcaa atg atg cag atc gta atg cag ggt ctt gat aat 533

Met Met Gln Ile Val Met Gln Gly Leu Asp Asn
1 5 10

gac ggc cct gtt aca gaa atg ctt gaa aac atg aac ggg aga cac ggt 581
Asp Gly Pro Val Thr Glu Met Leu Glu Asn Met Asn Gly Arg His Gly
15 20 25

gca aca aac gta aac aat cga gcg gga aac ggc aat ccc gtt cca aca 629
Ala Thr Asn Val Asn Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr
30 35 40

ggc gat gga act tac agc cgg gga gac atg aat tat cac aac cat ttg 677
Gly Asp Gly Thr Tyr Ser Arg Gly Asp Met Asn Tyr His Asn His Leu
45 50 55

gtg aat acg gcg gat aca ggc tat gac aga ccg gaa aac cgt aaa atc 725
Val Asn Thr Ala Asp Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile
60 65 70 75

tca agg aat atc act ggg cgc gtc aac aaa ttg aat tat gtt gac gaa 773
Ser Arg Asn Ile Thr Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu
80 85 90

agc cag gca gtc gta acg aat gaa acg gtc atc atc gcc gta cgg tct 821
Ser Gln Ala Val Val Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser
95 100 105

gat aaa agg ctg aca aat aac gag aga act caa att aga aaa gca gcc 869
Asp Lys Arg Leu Thr Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala
110 115 120

aaa aca ttt gcc gga gac cgg acc gtt caa gtt gtc gag gac gac ggc 917
Lys Thr Phe Ala Gly Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly
125 130 135

gca ttt aca agg ctg cgc gaa atg aac gat gat cct cag aac att agg 965
Ala Phe Thr Arg Leu Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg
140 145 150 155

gat cgc gga gac acg acg aat aac aat ttg aac cgc ttg cgg aac caa 1013
Asp Arg Gly Asp Thr Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
160 165 170

taacaagcag ggaattgccg gggattcccc ggcaattttt tataagcgct cggccgattc 1073

ctttacaaaa acggggaaaa ccgtataaag tgtacataga gacgagaatt attttggagg 1133

tagaaagtta tggctggcca ttctaaatgg aaaaatattc agagacgaaa aaatgcccaa 1193

gatgctaaac gcggcaaaat tttcatgaag cttgccaaag aaatatatgt agccgcgaaa 1253

gaagggggac cagatcccga atctaacgca agtctgcgtc tcgtcatcga taaagccaaa 1313

aatgcaaaca tgccaaatga caacatcgac cgcgccatca aaaaagcttc cggcagccag 1373

gatggaaaaa gctatgagga aattacgtat gagggctacg gaccaagcgg tgtggctgtc 1433

atggtcaaat gtttgacaga taataaaaac cggacggcga caagcgtcag aaccgctttc 1493

agcaaaaacg gcggcagctt ggg 1516

<210> 18
<211> 171
<212> PRT
<213> Bacillus licheniformis

<400> 18

Met Met Gln Ile Val Met Gln Gly Leu Asp Asn Asp Gly Pro Val Thr
1   5   10   15

Glu Met Leu Glu Asn Met Asn Gly Arg His Gly Ala Thr Asn Val Asn
            20   25   30

Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr Gly Asp Gly Thr Tyr
        35   40   45

Ser Arg Gly Asp Met Asn Tyr His Asn His Leu Val Asn Thr Ala Asp
    50   55   60

Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile Ser Arg Asn Ile Thr
65   70   75   80

Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu Ser Gln Ala Val Val
                85   90   95

Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser Asp Lys Arg Leu Thr
            100   105   110

Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala Lys Thr Phe Ala Gly
        115   120   125

Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly Ala Phe Thr Arg Leu
    130   135   140

Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg Asp Arg Gly Asp Thr
145   150   155   160

Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
                165   170

<210> 19
<211> 1249
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(746)

<400> 19
catcctttta caagtgccgc tcacccgttt atttgagagg tataaatcct taacaacaat 60

atcaattgga accgtttttt gcattttggg gaatatcggt ttttctatcg caaatggctg 120

gattgttttt atgctttcga tgtttgttct gacaatcggc gaaattttat gttttccttc 180

aatgaatgtc cttttggacg agctggctcc ggatcatatg aagggcgcgt attacggcat 240

gcaaaactta tacaacatcg gtgagttttt agggccttgg ctggggggaa tgatgcttgc 300

cttgtacggg ggaaaagccg tctttcttat tgctgcgtgt tcagtctttt tggctttagg 360

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cgcttaccat gtgggaagga gaaagttttt atctgcacag cattatggtg tatcgccttt      420

ttcttattga aaatttaggc cgcttatgca tgaatcatta agaattaccc aacctaaaag      480

gtaaaaaagg agtatgaatc atg gac aca aca ttg ggc tac ctc cgt gag tca      533
                      Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser
                      1               5                   10

ctg tcg aat cac ctt gaa cac ggc ata gga caa aac att tac aga aaa        581
Leu Ser Asn His Leu Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys
            15                  20                  25

atc gtt tcc ggg cga tat gcc aat gag gaa gag ttt gtc gag cac ttg        629
Ile Val Ser Gly Arg Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu
        30                  35                  40

gag gag cgg gaa atg gaa ttt ctg aat caa gtg ctt gaa cat gag atg        677
Glu Glu Arg Glu Met Glu Phe Leu Asn Gln Val Leu Glu His Glu Met
    45                  50                  55

aaa tat gcg ctg aat gaa cag gac cat aaa cgg aca aga gaa tta aac        725
Lys Tyr Ala Leu Asn Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn
60                  65                  70                  75

gaa gtg tat gaa ctg ctg ttt tgaaaggcgg gaatgatcaa tgggtgcaat           776
Glu Val Tyr Glu Leu Leu Phe
                80

agagcggaac ggatacacgt ttgaaccgga atacagcgtg accagacaaa acggtgcgat      836

ccatgtatac cggcgcggcc ggtttgtcga ggagattccc tttgagtttc acggggagtt      896

tccagagcat gatttaattg aagagcttgt caatcattat tgttatgaaa ataaaatata      956

aggcttgaag aggctgccga ccgggcggct tttatttttg gatttttata tctataatcc     1016

gcttgcagtt ttttagaacg gcagcagaaa agctgccata aatatgacag ctcatgcatc     1076

gctatttttt cttttcgtcg tagtattgaa cagggtacat ggatccttcc gataccattt     1136

tgttatcttc gatatcatgc ggagacgggt gtcctgcttt ttcaaccggg aatgaatcta     1196

cgttgtgttt ttccgaaaag taagggatct ttctttgac gttttgcaag tac             1249


<210>  20
<211>  82
<212>  PRT
<213>  Bacillus licheniformis

<400>  20

Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser Leu Ser Asn His Leu
1               5                   10                  15

Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys Ile Val Ser Gly Arg
            20                  25                  30

Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu Glu Glu Arg Glu Met
        35                  40                  45

Glu Phe Leu Asn Gln Val Leu Glu His Glu Met Lys Tyr Ala Leu Asn
    50                  55                  60
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Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn Glu Val Tyr Glu Leu
65 70 75 80

Leu Phe

<210> 21
<211> 1620
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1121)

<400> 21
cttcgtgaaa aatacagttc taaagatcaa aaaacgcagc agaagcttca acaggaaacg 60

atggctctca tgcagaagca cggggttaac ccgcttgccg gatgtttccc gatcttaatt 120

caaatgccga ttttaatcgg attctatcat gccattatga gaacgcggga aatcgcagaa 180

cacagctttt tatggtttga ccttggggag cgtgatccgt atttcatttt gccgattctc 240

gccggtgtgt tcacattcat tcagcaaaag ctgatgatgg cgggaacagc gcagcaaaat 300

ccgcagatgg cgatgatgct ttggctgatg ccgatcatga tcgttgtatt tgcgatcagt 360

ttcccggcgg ctctttccct gtactgggta gtcggtaact tattcatgat tgctcaaacc 420

ttctttatca aagggcctga tctaaaggct gagagacagg aagcggcagc cggaggaaaa 480

aaatccggag gtaagaaaaa gtg aag gaa ctg act gct act gga cgt acc gtc 533
Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val
1 5 10

gat gaa gca gtg caa tcc ggg ctt gaa cag ctg ggc ctt cat gca gat 581
Asp Glu Ala Val Gln Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp
15 20 25

gat gtc gaa gtc gac gta gtt gat gaa gga aaa aag gga tta ttc ggc 629
Asp Val Glu Val Asp Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly
30 35 40

att ttc ggt cat cgg tct gca gtc gtg aac att cgg gaa aaa ata gac 677
Ile Phe Gly His Arg Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp
45 50 55

ccg gtt aaa gaa gca aaa caa tat ttg gaa aat gta att tcg aat atg 725
Pro Val Lys Glu Ala Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met
60 65 70 75

gga ata caa gcc cag gtg acg gca gaa gag gag tct aaa cga gtg gtt 773
Gly Ile Gln Ala Gln Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val
80 85 90

ttt cag ttg aaa gga gac aaa aca gct ctt tta att gga aaa agg gga 821
Phe Gln Leu Lys Gly Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly
95 100 105

caa act tta aat gcc ctt gaa acg ctg acg cag ctc gtg ctc aat cgt 869
Gln Thr Leu Asn Ala Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg
110 115 120

cat tcc gac aga tat atc caa gcg gtg gtt gac gcc gaa gga tac cgc 917

His Ser Asp Arg Tyr Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg
125 130 135

gca aag cgg aag gaa aca ctt gct cag ctg gca ttg aag ctt gct gac 965
Ala Lys Arg Lys Glu Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp
140 145 150 155

cag gcg gcc agg cag aaa aaa gac att cac ctg gag ccg atg cct tcc 1013
Gln Ala Ala Arg Gln Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser
160 165 170

agt gag cgc aag gtc atc cat gat acg ctt gcg ggc tac tcg cag cat 1061
Ser Glu Arg Lys Val Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His
175 180 185

atc gaa act tac tct acc ggt gaa gac cat aac cgg cac ctt gtc atc 1109
Ile Glu Thr Tyr Ser Thr Gly Glu Asp His Asn Arg His Leu Val Ile
190 195 200

tca tat aaa aaa taacatgaaa accgaagttc ccaaaattgg ggcttcggtt 1161
Ser Tyr Lys Lys
205

tttttgccgt tgaaaatcga tgaaatgcag caaaatcagt ttaagttcta ttttttcagg 1221

cgtaagctgt tgatgaaaat gaaatttaat tgttattcac atgtggataa gttaaagtaa 1281

gtaatgatgg cttagaacgg ttgtggataa cggttcaagt cacttccact tcaattgaaa 1341

ctatgttatc tttaaatttt gattacaata aaagtttttc atccgtatac gatgtttgga 1401

agatgacccg gcaaatgggg ataatagata taggaatgaa aaagagaggt gaaagccatg 1461

gataccatcg ctgcgatttc aacgccgatg ggagaagggg cgattgcgat cgtccggatg 1521

agcggccctg aggctcttgc gatcgccgat aaagtgtata aaggacctcg cggaaaaagg 1581

ctgagttccg tcgattcaca tacgattaac tacggtcat 1620

<210> 22
<211> 207
<212> PRT
<213> Bacillus licheniformis

<400> 22

Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val Asp Glu Ala Val Gln
1 5 10 15

Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp Asp Val Glu Val Asp
20 25 30

Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly Ile Phe Gly His Arg
35 40 45

Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp Pro Val Lys Glu Ala
50 55 60

Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met Gly Ile Gln Ala Gln
65 70 75 80

Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val Phe Gln Leu Lys Gly

85 90 95

Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly Gln Thr Leu Asn Ala
100 105 110

Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg His Ser Asp Arg Tyr
115 120 125

Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg Ala Lys Arg Lys Glu
130 135 140

Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp Gln Ala Ala Arg Gln
145 150 155 160

Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser Ser Glu Arg Lys Val
165 170 175

Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His Ile Glu Thr Tyr Ser
180 185 190

Thr Gly Glu Asp His Asn Arg His Leu Val Ile Ser Tyr Lys Lys
195 200 205

<210> 23
<211> 1614
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1115)

<400> 23
gtgtttatcg ccgaaccttc cccaaaaagg agaaactaaa aaggccatca aaaatgtgac 60

gccgaaaacg tatccgctcc attttgccgt aaatccgtcc gaatagctgc caagcgtctc 120

aatatagagg gaaagaaacg gcagaaccat tgtggagctt gcggccacga aaaaattcgc 180

aaaccacatg atcacaaggt ttttcttata aacagagatg cgaatcacct tcttaaaaaa 240

tttgaattcc ctttcattat aaatgaaatg cgaaagctgc atggaattga tgctctatag 300

aatgacgaaa aatgggcatt tgaaggaatt ttcaacattt tcagaaaata aaaccttaaa 360

tatagaaata taatgatata ataagagaaa tatgagcgta ctttggaaaa cattcagaag 420

actataggct tggataattt caatccgctg cgttaccacc ataagttttt tatattgaga 480

tagaaaggca ggtgtgaaag ttg gaa gcg agc acc tta ctg att att gat ttt 533
Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe
1 5 10

gaa ttt aca atg cct gag gga aag tat cac ccg caa aat ttt ttc ccg 581
Glu Phe Thr Met Pro Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro
15 20 25

gaa atc ata gaa gca ggg att gta aag acg gtt cat gat gag gtg gtt 629
Glu Ile Ile Glu Ala Gly Ile Val Lys Thr Val His Asp Glu Val Val

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        30                  35                  40

gag acg ttt tca agc tat att aag ccg aag aag ttc cct aaa tta acg        677
Glu Thr Phe Ser Ser Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr
    45                  50                  55

agg cgc tgc aaa aat ttt ctc agc atc acg cag gaa cag gtt gac caa        725
Arg Arg Cys Lys Asn Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln
60                  65                  70                  75

ggc atc acg ttt aac gcg ctg att gaa aag ctg cgg gag ctt gat cct        773
Gly Ile Thr Phe Asn Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro
                80                  85                  90

gac cga aac agc gtc atc att aca tgg gga aac atg gat atg aaa gtg        821
Asp Arg Asn Ser Val Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val
            95                  100                 105

ctg aag caa aat tgc atg ttc aac cat gtt ccg ttt ccg ttt aaa gga        869
Leu Lys Gln Asn Cys Met Phe Asn His Val Pro Phe Pro Phe Lys Gly
        110                 115                 120

gag atg agg gac ctt tcc atg gag tac aag gaa ttt ttc ggc gac aaa        917
Glu Met Arg Asp Leu Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys
    125                 130                 135

aca ttg acg aat ttg tgg aag gca gcg gaa gag tac ggc gat tca gga        965
Thr Leu Thr Asn Leu Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly
140                 145                 150                 155

acg gga aaa cag cat aaa gcg ctt gac gac gcg atg aca acg tat aag       1013
Thr Gly Lys Gln His Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys
                160                 165                 170

ttg ttt cgg ctc gta gaa cgg gat aag aag tat ttg gaa aat ccg aag       1061
Leu Phe Arg Leu Val Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys
            175                 180                 185

ccg acg acg atc ggc gaa cgg gtt gac ctc tca aaa gtc ttt ccg cac       1109
Pro Thr Thr Ile Gly Glu Arg Val Asp Leu Ser Lys Val Phe Pro His
        190                 195                 200

gcc aca taaaaaccc aatctgacaa acagattggg ttatttgtgc aggaaatatt         1165
Ala Thr
    205

cttttcaag cccatgaata agctcaagcg attttgccgc gtattcggac gaatcgtttt      1225

gcagatccgt ttttaagcgg ctcaaagctg agcggagcga atccgcataa tccggtacag     1285

cttcatcgaa cggcttcacc atgcggtgcg ggatattcgt ctgttcaccg taagcgagcg     1345

cttttcgttc atgaaaaaaa gggacgtctg cccgattggg atgatgaagg tcgccctgct     1405

tcggatgggt cagcacggcg aggattttga ccaggtagtg catcggttta acatccgtaa     1465

tttcgccgat gtagacgcct gttttataaa agccctttac gcgatctccg acttgaaatt     1525

ggttgttcac tgcatctgcc tcctaatggt atcataataa ataaatggta aaaaaatcat     1585

ttcagggagg aagaaaaatg gcgccgttt                                       1614
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<210> 24
<211> 205
<212> PRT
<213> Bacillus licheniformis

<400> 24

Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe Glu Phe Thr Met Pro
1   5   10   15

Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro Glu Ile Ile Glu Ala
            20   25   30

Gly Ile Val Lys Thr Val His Asp Glu Val Val Glu Thr Phe Ser Ser
        35   40   45

Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr Arg Arg Cys Lys Asn
    50   55   60

Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln Gly Ile Thr Phe Asn
65   70   75   80

Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro Asp Arg Asn Ser Val
                85   90   95

Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val Leu Lys Gln Asn Cys
            100   105   110

Met Phe Asn His Val Pro Phe Pro Phe Lys Gly Glu Met Arg Asp Leu
        115   120   125

Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys Thr Leu Thr Asn Leu
    130   135   140

Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly Thr Gly Lys Gln His
145   150   155   160

Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys Leu Phe Arg Leu Val
                165   170   175

Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys Pro Thr Thr Ile Gly
            180   185   190

Glu Arg Val Asp Leu Ser Lys Val Phe Pro His Ala Thr
        195   200   205

<210> 25
<211> 1600
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1097)

<400> 25
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tgttcatttt gaagtgtttt ggcaaagcct tcagcgaatt ttggatcttc aaagactttt 120

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ttccaaaatt cagctccttt tttggaggtc attgtttttt caacggtttc tttgacagtt     180

ttttcatcca ttacaagtgt ttcatttaat ttgtcatcat ttaatatttc ttgaatcgct     240

tttttccgt catctgtctt taatatatcg acaaccattt ttttggtttg atcatagtcc     300

atctcagctg cttggtccgt gggagcacaa gctgttacag atagaaacag aaaacagctt     360

atcgatagca ttgcggtctt gaacatgctt aagctccttt cgaaaactcg tcttaccttt     420

aatatgaatg tcttttaaaa atttatacat aacaaaatat cgctgttaca gcggtttatt     480

taggggttgg gaagtctaca atg aaa agc cgt aat ctc gtc cga ttt ttc ttt     533
                      Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe
                      1               5                   10

tcc gta ttg ggt gtc gga gct ttg act aca agt att gtc ggt ttt gcc       581
Ser Val Leu Gly Val Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala
            15                  20                  25

ata gag tgg gga aga tat aag gag ctg ttt ctt tcc ttc gag gta ttg       629
Ile Glu Trp Gly Arg Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu
        30                  35                  40

gag att ctg tct gtt ctt ttc tgg ttt atc ggg gtt ggc atg atc ttt       677
Glu Ile Leu Ser Val Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe
    45                  50                  55

agc gtg att gct caa atg gga ttt gtg att ttc tta acg att cac cgc       725
Ser Val Ile Ala Gln Met Gly Phe Val Ile Phe Leu Thr Ile His Arg
60                  65                  70                  75

ttt gca ctg gaa att ttc aga tct cat tct ttg tgg aat tcg att cag       773
Phe Ala Leu Glu Ile Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln
                80                  85                  90

ctg ttt ttg att ata ttt gtc gcg ttt gac ttg gtt tac ttg cgc ttt       821
Leu Phe Leu Ile Ile Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe
            95                  100                 105

ctg ttt ttt gaa aaa gat gga ggc tcc atc att ccg tac att tgg ctg       869
Leu Phe Phe Glu Lys Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu
        110                 115                 120

ccg ctc ttt att ttg gcg gta ggc att gcg gcc gct tat gca aag caa       917
Pro Leu Phe Ile Leu Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln
    125                 130                 135

aaa cag tcc tct aaa aaa acg ttc gtt tcc gca tta ttt cta atg ttt       965
Lys Gln Ser Ser Lys Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe
140                 145                 150                 155

gtt ttt act gtg atg gag tgg ttc ccg gcg tta agg gtc aat gaa gag      1013
Val Phe Thr Val Met Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu
                160                 165                 170

gac tgg ctc tat tta atg ctg ctt cct tta tta gcc tgc aac gct ttt      1061
Asp Trp Leu Tyr Leu Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe
            175                 180                 185

cag ctt tta atg ctg cca aaa ttt cag gca cgc gct tagaccggct           1107
Gln Leu Leu Met Leu Pro Lys Phe Gln Ala Arg Ala
        190                 195

gctactttac ttctgaagat tttgcatccg tatttgcgat taattcgctg actgttacgt    1167

ttttgagccc cttgcttctg agatggtgca cgatctctgg cagggcttct tttgtttgtt    1227
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tggcggaatc tgaagcgtga aagagcacga tgtcaccggc gtttaccgtt ccatttacgt 1287

tttggacgat cttttgaacc cccgggttcg tccagtcatc cgagttaata ctataatgaa 1347

caacggtgta gccgtactgt ttagcaacat cgagtacgtc tttattaaac tggccggtcg 1407

gcggtcttaa aagcgtaagg tcgtcaagcc cgagtttttg aaaggagtgt cgtgcttttg 1467

ctaagtcttt tttgatctcg cttttcttca tttgcgaata gtttttataa gcatagccca 1527

tactcccgat ctggtgacca tctttacgga ttctttctac gacatccggg tggcgctctg 1587

cccatgaagc tga 1600

<210> 26
<211> 199
<212> PRT
<213> Bacillus licheniformis

<400> 26

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Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala Ile Glu Trp Gly Arg
20 25 30

Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu Glu Ile Leu Ser Val
35 40 45

Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe Ser Val Ile Ala Gln
50 55 60

Met Gly Phe Val Ile Phe Leu Thr Ile His Arg Phe Ala Leu Glu Ile
65 70 75 80

Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln Leu Phe Leu Ile Ile
85 90 95

Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe Leu Phe Phe Glu Lys
100 105 110

Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu Pro Leu Phe Ile Leu
115 120 125

Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln Lys Gln Ser Ser Lys
130 135 140

Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe Val Phe Thr Val Met
145 150 155 160

Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu Asp Trp Leu Tyr Leu
165 170 175

Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe Gln Leu Leu Met Leu

180 185 190

Pro Lys Phe Gln Ala Arg Ala
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<210> 27
<211> 1991
<212> DNA
<213> Bacillus licheniformis

<220>
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<222> (489)..(1499)

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gaagtggccg acatcaacgg cctgactgca caggaagtca tcgatattca cacctcgggt 180

gagtacctcg tttatatgat cggctttgcg ccgggcttcc cttacctagg cggaatgtct 240

gaaaagatag ccgcaccgcg gcggtcatct cctcggactt cgattcccgc cggttcagtc 300

ggaatagccg gcatgcaaac aggcgtctat ccccttcaa cgccgggcgg ctggcagctg 360

atcggcaata cgccgcttga attattcaag ccttatgaac agcctccgag ccttctgaga 420

gcaggggata tcgtgaaatt tgtcagcgtg acagaagagg agtatcacgc gctgaaggag 480

gggaaatc ttg agc ata gaa gtg tta aag ccg ggt ctg atg aca acg gtt 530
Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val
1 5 10

caa gac ttg ggc cgc aca ggt ttt caa aaa tac ggc gtg ctt gtc agc 578
Gln Asp Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser
15 20 25 30

ggt gcc atg gat gcc gat tct ttg cgg att gcc aat ctg ctc gcg ggg 626
Gly Ala Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly
35 40 45

aac agc cag aac gaa gct gcg ctt gaa gtg acg ctg atg ggg ccg ggg 674
Asn Ser Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly
50 55 60

ccg tct ctc cgc ttt caa aaa cct gct ctt ata gcg gtg acg ggc gct 722
Pro Ser Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala
65 70 75

gac ttt tca ctg atg gta aat gac gaa gaa gtc ccg ctt tgg cgc ccg 770
Asp Phe Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro
80 85 90

gtt ttc atc aaa gag ggc agc gtg ttg aca ttc ggc atg tgc aag cgc 818
Val Phe Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg
95 100 105 110

gga agc cgt gca tat atg gca gtg gcc ggg gga att gat gtg ccg cct 866
Gly Ser Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro
115 120 125

gta atg gaa agc aaa agc aca tat gtc aga gca gga ctc ggc ggc ttt 914
Val Met Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe

130 135 140

caa gga agg gcg ctt caa aag gga gac gtg tta tcg cta ggc agc ccg 962
Gln Gly Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro
145 150 155

acg ccg ttg tcg gaa gcg ctg cac aga aag ctc gca gac gag ggc aaa 1010
Thr Pro Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys
160 165 170

gaa cgg ggc ttt gcg gct ccg aag tgg gct gtc gac cgc aaa tat ttt 1058
Glu Arg Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe
175 180 185 190

ctc ccg cta aaa aag aac ccg gtc att cgt gtc atc aaa ggc gat cag 1106
Leu Pro Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln
195 200 205

ttt gct tgc ttt acc tca tca tca caa gag cgc ttt ttc gcg ggt cca 1154
Phe Ala Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro
210 215 220

ttc cgg gtg acg gct aaa tcc gac cgg atg ggg tac cgt ctt caa gga 1202
Phe Arg Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly
225 230 235

gag gcg ctc gaa ctc act cag cct ctg gaa atg atc tct gaa gcg gta 1250
Glu Ala Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val
240 245 250

tca ttc gga acg att caa gtg ccg ccc gac ggc aat ccg atc gtt ctt 1298
Ser Phe Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu
255 260 265 270

ctc gca gac agg cag aca gcg ggc gga tac ccg aga atc gcc cat atc 1346
Leu Ala Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile
275 280 285

gca tca gct gat ttt tct cag gtc acg cag atg atg ccg ggc gag cag 1394
Ala Ser Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln
290 295 300

gtg cag ttt cag ctt gtc agc ctt cag gaa gca gag cgc gtt tac atc 1442
Val Gln Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile
305 310 315

gaa cgg gag acg aaa atc agc gaa ctt tct gcc cga ttg aag ctt gaa 1490
Glu Arg Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu
320 325 330

tac atg tta tgataggtgt gatgtgtatc aggaggggga aggcatggaa 1539
Tyr Met Leu
335

cataaaaaca aaacagtcgt caaagccatg accctgctca atctgttcct gacgagagaa 1599

aggctctcgc tgggcgacat gattgagctg acaggcatgc cgaaaacatc tgtctaccgc 1659

atggtttgtt ctctcgaaga aatgggtttt ctcgaccgcg acgagaacgg gatgtatagc 1719

ttaggactgc tgtttttgca atacggccac cttgtttcag aaaggcttga tattcgaaaa 1779

atcgctctgc ccatcatgga agaactccgc gatgacgtgg atgaagccgt ccatttaatt 1839

gtaaggcagg gaaatgaagc aatgtatata gaaaaaattg agggcacgca gaccgttcgc 1899

ctctatacag cgatcgggag gcggtcccct ttatatgccg gagcctgtgc gagaagcatt 1959

ctgacgtttt tgcctgaaga ggagcgggat gc 1991

<210> 28
<211> 337
<212> PRT
<213> Bacillus licheniformis

<400> 28

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20 25 30

Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly Asn Ser
35 40 45

Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly Pro Ser
50 55 60

Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala Asp Phe
65 70 75 80

Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro Val Phe
85 90 95

Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg Gly Ser
100 105 110

Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro Val Met
115 120 125

Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe Gln Gly
130 135 140

Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro Thr Pro
145 150 155 160

Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys Glu Arg
165 170 175

Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe Leu Pro
180 185 190

Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln Phe Ala
195 200 205

Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro Phe Arg
210 215 220

Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly Glu Ala
225 230 235 240

Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val Ser Phe
245 250 255

Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu Leu Ala
260 265 270

Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile Ala Ser
275 280 285

Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln Val Gln
290 295 300

Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile Glu Arg
305 310 315 320

Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu Tyr Met
325 330 335

Leu

<210> 29
<211> 2287
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1784)

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tatgagctgc ttacatttaa ctggatggcc cattcgctga cgcttgaata tgaggtgatc 180
ggtcaagtca aggatttgtc agcttatgaa gaaaggctcg tcgttctcat cagaaagctg 240
tttgggattt ttgacgatgc cgttttgaaa ggcagcgaca atcatctgac gatcacgctg 300
cagacggacg gtccggacga ccgcctcgtc atctttctcg atttccacgg cgtattcaca 360
aagctgaccg gtatcaaaga ctttcatcat tcactggccg acttttatga aatcaagcgg 420
tttgatgtaa cagaccgtga gtgcatcgcc gaaattcata tcaagtaaag cggtttttta 480
ggaatagaac ggaggacatt atg ttt gtt gat cag gtg aaa ata tac gta aaa 533
Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys
1 5 10

ggc gga gac gga ggc aac ggt atg gtt gct ttc cgc cgc gaa aaa tat 581
Gly Gly Asp Gly Gly Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr
15 20 25

gtg cca aaa gga ggc cct gcc gga ggt gac ggc gga aaa ggc gga gac 629
Val Pro Lys Gly Gly Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp
30 35 40

gtc gtt ttc aaa gtt gac gaa ggt ctc agc acg ctg atg gat ttt aga 677
Val Val Phe Lys Val Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg
45 50 55

tat caa aga cat ttt aag gca gcg cgc gga gaa cac ggc atg tct aaa 725
Tyr Gln Arg His Phe Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys
60 65 70 75

aac cag cac ggc cga aat gcc gaa gac atg gtt gtg aaa gtc ccg ccc 773
Asn Gln His Gly Arg Asn Ala Glu Asp Met Val Val Lys Val Pro Pro
80 85 90

ggc acg gtt gtc att gac gat gat aca aaa cag gtc atc gct gat tta 821
Gly Thr Val Val Ile Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu
95 100 105

acg gag cac gga cag gaa gcc gtc atc gca aaa ggg gga cgc ggc gga 869
Thr Glu His Gly Gln Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly
110 115 120

cgg ggc aat aca cgt ttt gcg acg cct gcc aac ccg gcg ccg cag ctt 917
Arg Gly Asn Thr Arg Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu
125 130 135

tct gaa aac ggc gaa ccc ggc aag gag cgc tat att gtt ctc gag ctg 965
Ser Glu Asn Gly Glu Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu
140 145 150 155

aaa gtt ttg gca gat gtc ggt ctt gtc ggc ttc cca agc gtc gga aaa 1013
Lys Val Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys
160 165 170

tca acg ctc ctg tct gtc gtg tct tcg gcc aag ccg aaa att gcc gat 1061
Ser Thr Leu Leu Ser Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp
175 180 185

tac cac ttt aca acg ctg aac ccg aat ctc gga atg gtc gaa acg gaa 1109
Tyr His Phe Thr Thr Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu
190 195 200

gac ggc cgc agc ttt gta atg gcg gat ctt ccg gga ctg att gag ggg 1157
Asp Gly Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly
205 210 215

gcg cac gaa gga gtt ggc ctc gga cac caa ttc ctc agg cat atc gaa 1205
Ala His Glu Gly Val Gly Leu Gly His Gln Phe Leu Arg His Ile Glu
220 225 230 235

aga acg cgc gtc atc gtg cac gtt att gac atg tcg ggt ctt gaa ggg 1253
Arg Thr Arg Val Ile Val His Val Ile Asp Met Ser Gly Leu Glu Gly
240 245 250

cgc gac ccg tat gaa gat tat gtg acc att aat aaa gag ctt gaa cag 1301
Arg Asp Pro Tyr Glu Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln
255 260 265

tat aat ctc agg ctg aca gaa cgt cct caa att att gtc gcc aat aaa 1349
Tyr Asn Leu Arg Leu Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys
270 275 280

atg gat atg ccg gat gcg gaa gaa aat ctg aag gct ttc aaa gaa aag 1397
Met Asp Met Pro Asp Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys
285 290 295

ctc aca gat gat tat cct gtt ttt cca atc agc gcg gtg acc aga caa 1445
Leu Thr Asp Asp Tyr Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln
300 305 310 315

10295.204.ST25.txt

ggc ttg agg gat ctg ctg ttt gaa att gcc gac cgt ttg gaa acg acg 1493
Gly Leu Arg Asp Leu Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr
320 325 330

ccg gaa ttc ccg ctc tac gac gaa gaa gac atg gct gaa aac aga gtc 1541
Pro Glu Phe Pro Leu Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val
335 340 345

atg tat aag ctt gag gat gag gaa gcg ccg ttt gag atc agc cgt gat 1589
Met Tyr Lys Leu Glu Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp
350 355 360

cct gac ggc acc ttc gtg ctc agc gga gcc aag ctt gaa cgc tta ttt 1637
Pro Asp Gly Thr Phe Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe
365 370 375

aaa atg acg gac ttt tca aga gat gag tct gtt aag cgt ttt gcc aga 1685
Lys Met Thr Asp Phe Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg
380 385 390 395

cag ctt cgc gga atg ggc gtc gat gat gcg ctt cgg gcc cgc ggt gca 1733
Gln Leu Arg Gly Met Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala
400 405 410

aaa gac ggg gat acg atc cgt ctt ctc gaa ttt gaa ttt gaa ttt atc 1781
Lys Asp Gly Asp Thr Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile
415 420 425

gac tgatcatacc ggagagtttg ccaagcaagc tctccgactt ttagctgaaa 1834
Asp

ggaacgccct tcctttcgca ggatcaatgt aaaggaatca gggtttttaa aaggagagaa 1894
aagtctgtga aagaggagac cttttatctt gtcagggaag acgtgctgcc ggaggcaatg 1954
cggaaaacac ttgaggtcaa aaagctgatt gagcggaaaa aagcggaatc tgtagctgaa 2014
gccgtacaaa aggtagattt gagccgaagc gctttttata agtacagaga tgcggttttt 2074
cctttttata cgatggtcaa ggaacagatt atcacgcttt tttttcattt ggaggaccgc 2134
tcaggaacgc tgtcccatct gctgcaagtg gtagctgaat cgggctgcaa tgtgctgtcg 2194
atccaccaga ccatccctct tcaaggaaga gcgaatgtca cgctctctgt cagtacgaga 2254
ggcatggatg aaaatatcga tttgctgatg aac 2287

<210> 30
<211> 428
<212> PRT
<213> Bacillus licheniformis

<400> 30

Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
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Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
35 40 45

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
    50   55   60

Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
65   70   75   80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
                85   90   95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
            100   105   110

Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
        115   120   125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
    130   135   140

Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu Lys Val Leu Ala Asp
145   150   155   160

Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Ser
                165   170   175

Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp Tyr His Phe Thr Thr
            180   185   190

Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu Asp Gly Arg Ser Phe
        195   200   205

Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala His Glu Gly Val
    210   215   220

Gly Leu Gly His Gln Phe Leu Arg His Ile Glu Arg Thr Arg Val Ile
225   230   235   240

Val His Val Ile Asp Met Ser Gly Leu Glu Gly Arg Asp Pro Tyr Glu
                245   250   255

Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln Tyr Asn Leu Arg Leu
            260   265   270

Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys Met Asp Met Pro Asp
        275   280   285

Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys Leu Thr Asp Asp Tyr
    290   295   300

Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln Gly Leu Arg Asp Leu
305   310   315   320

Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr Pro Glu Phe Pro Leu
325 330 335

Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val Met Tyr Lys Leu Glu
340 345 350

Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp Pro Asp Gly Thr Phe
355 360 365

Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe Lys Met Thr Asp Phe
370 375 380

Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg Gln Leu Arg Gly Met
385 390 395 400

Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala Lys Asp Gly Asp Thr
405 410 415

Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile Asp
420 425

<210> 31
<211> 2115
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1616)

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atgtgatgcc ctcaacagcc tttttgactt tggcgatttc gtctgattgt tgttttaatt 120
gttccagcgt ttgatctatt gcattgtgca gcgcctgaac atcaagagtc ttcatggcat 180
tctcctctaa tccttttcat tacaatcagt atatagttta ccactttata gaaagtactt 240
ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatttctat 300
tgattcattt cgattaccgt aaacaagttt gttgtagcat tctttaggct ctgtgactaa 360
accaaaaagc catttgtttt aaattggtct ttcggtatca cgaaaatttc gtttttttggg 420
ctgatagaag ttttgcaatt atgaattgta tgttaatctt taacataaaa aggatgttag 480
ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc 533
Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile
1 5 10

aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa 581
Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu
15 20 25

gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa 629
Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu
30 35 40

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gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat      677
Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His
    45                  50                  55

gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa      725
Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys
60                  65                  70                  75

tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc      773
Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly
                80                  85                  90

ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct      821
Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser
            95                  100                 105

cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa      869
Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys
        110                 115                 120

aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat      917
Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr
    125                 130                 135

aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg      965
Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met
140                 145                 150                 155

tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat      1013
Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr
                160                 165                 170

gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att      1061
Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile
            175                 180                 185

gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag      1109
Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys
        190                 195                 200

gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt      1157
Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu
    205                 210                 215

tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct      1205
Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala
220                 225                 230                 235

att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca      1253
Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala
                240                 245                 250

aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga      1301
Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg
            255                 260                 265

aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa      1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu
        270                 275                 280

agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt      1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val
    285                 290                 295

tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa      1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu
300                 305                 310                 315
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aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa 1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu
320 325 330

ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat 1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn
335 340 345

gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc 1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile
350 355 360

aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga 1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile
365 370

cccttgcttt gggcttgttg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac 1696

aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcaggtcat 1756

gtgatggcct gcctttttgg tgaaagaatt attttagttt gaaaaccaga acgattgtgt 1816

taatactcat ctttcttcgt cccttgtgtt ggaattttca tcatatcaat atttgaatat 1876

gcggctgtcc gcattattaa caattttaaa ttttttgcac aaattttata caaaggcaga 1936

caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc 1996

taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt 2056

ttattcctca tcaaagcgga gagccgccaa cataaacgca atgaccaact gttgtccgc 2115

<210> 32
<211> 372
<212> PRT
<213> Bacillus licheniformis

<400> 32

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp
1 5 10 15

Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
100 105 110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
145 150 155 160

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
355 360 365

Leu Tyr Glu Ile
370

<210> 33
<211> 2077
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1574)

<400> 33
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aaatattatg gtctttttcc tactttaaca aggcataatc tttccctcta ttgaatgtaa     120

tatagtaaag cgaatagagg agggtataca aatgaatcct tactatatga tgctcttatg     180

ttatgtccta tcgatcatcc actttttaat aggctaccgg gaagccctga aaataagcgg     240

ggttgacggg ctggtcaacg gaaccgcaat gatctcctgt attccgcttg gcgcggtttt     300

cgctttttc gcgcactttt tttggaaaat gacgatttaa tttcgggaat gaatttttc      360

gccaacaaac atgcatttcc gtgttattca cagacggcgg cagtttatgc tatgattaat     420

agaacttcaa tttacaaaaa attcacaaag attggaggga aaagaatggc caaagccggg     480

cttctcaaga agtcgccaat atg ctg aac gac tgg tac ata ctg atg aaa aaa     533
                      Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys
                      1               5                   10

cga gac att tca ggt tca atc gaa atg aaa gat gac ata gat aaa gca       581
Arg Asp Ile Ser Gly Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala
            15                  20                  25

att gaa aag atg gaa gaa gat cat gac gtt ctt ctc tat tat caa atg       629
Ile Glu Lys Met Glu Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met
        30                  35                  40

ctg gat ttt cgc tta agg ctt ctt ctt gaa gat atc tcc caa tct tcc       677
Leu Asp Phe Arg Leu Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser
    45                  50                  55

aca gaa aaa ttg gaa gcc atc agt ttt aag gac aaa gat cca aaa agt       725
Thr Glu Lys Leu Glu Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser
60                  65                  70                  75

acg gac gat aag ctg aat tat tat ttt tat ctg ttc aaa ggg att tat       773
Thr Asp Asp Lys Leu Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr
                80                  85                  90

gaa gac tac aag caa aac cat aca gaa gcg ctt aat ttt ttc aga ata       821
Glu Asp Tyr Lys Gln Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile
            95                  100                 105

gcg gaa aaa agg ctg agc gtc att caa aat gaa att gaa aaa gcc gaa       869
Ala Glu Lys Arg Leu Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu
        110                 115                 120

ttt cat tat aaa atc ggt gtt ttg tat tac aac tta aaa gcg aca tgg       917
Phe His Tyr Lys Ile Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp
    125                 130                 135

ctg tcg att cac cac atc aac att gcc tca ggc atc ttc caa ggg tat       965
Leu Ser Ile His His Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr
140                 145                 150                 155

gac ggg tat gcc aag cgg gtc atc aac tgc aaa atg ctg atc ggg ctc      1013
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Asp Gly Tyr Ala Lys Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu
                160                 165                 170

aat tat att gac caa ttt aag ttt gcc gaa agt gaa gta ttg tta aag     1061
Asn Tyr Ile Asp Gln Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys
            175                 180                 185

gaa gca att gaa aaa acc gaa aaa atc ggc gac caa tat ctt ttg cct     1109
Glu Ala Ile Glu Lys Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro
        190                 195                 200

tat acc tac tat aat atg ggc ttt ttg aag agt aag gaa gat aaa cac     1157
Tyr Thr Tyr Tyr Asn Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His
    205                 210                 215

gaa gaa gcg ctg aag tat tat aat aaa gct ttt gca atc aaa gac ttt     1205
Glu Glu Ala Leu Lys Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe
220                 225                 230                 235

gaa acg aaa gcc aag tat gct tac ctt cta tgt gta tat gaa aac aca     1253
Glu Thr Lys Ala Lys Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr
                240                 245                 250

agg tct ctt ttc aaa acc aac gat ccc gac caa gct ttt aaa tgg atc     1301
Arg Ser Leu Phe Lys Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile
            255                 260                 265

gac aca ggc ttt aaa aaa gct caa gaa gtg aat agc gaa att ttc gaa     1349
Asp Thr Gly Phe Lys Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu
        270                 275                 280

tta aaa ttc aaa act tta tat aca tta cat tcc gat tgt cag aat aaa     1397
Leu Lys Phe Lys Thr Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys
    285                 290                 295

ctg gaa gta atc aag gac ttt att cac caa tta gaa gat aaa aaa gca     1445
Leu Glu Val Ile Lys Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala
300                 305                 310                 315

tgg gtt gat ctg gag gaa ttg ctg atg gac gta gcg aat tac tat agg     1493
Trp Val Asp Leu Glu Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg
                320                 325                 330

gaa aat aag tta tac gaa gaa gcc ata tat ttc tac att aaa aca gac     1541
Glu Asn Lys Leu Tyr Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp
            335                 340                 345

aag gca agt aaa ctt gcc gga aga gga gga gaa taggatgaaa aaagtgttgt   1594
Lys Ala Ser Lys Leu Ala Gly Arg Gly Gly Glu
        350                 355

tagctgtatt tgtattaggc actgttttca gcttttcgtt tgcaaatcac gctcctgaag   1654

cggcttccca aagcaatgag atacttttgg cttctcgtgg agcaggcggg tgactacatc   1714

ctcaaaatac ccattcagac atctgctgaa tgggtatttt gcactttaca ttcatattca   1774

ggagtgatcg atatgggaaa gaaagtactg ctgacaggat ttgacccctt tgggggagaa   1834

acagtcaatc cgtcctggga agctgtaaaa cggctgaacg gagaggaagc agaaggcgtc   1894

tctatcgcag cggagcagat tccgaccgtt tttcatcatt cagcggccgt tttgaaaaaa   1954

gcgatcgaaa agcacaaacc cgatgtcgtc atttgcgcag ggcaagcagg cggcagggct   2014

catattacgc cggaacgcat cgcaatcaac atcgatgatg ctcgcattcc ggataatgaa   2074

gac                                                                 2077
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<210> 34
<211> 358
<212> PRT
<213> Bacillus licheniformis

<400> 34

Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys Arg Asp Ile Ser Gly
1   5   10   15

Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala Ile Glu Lys Met Glu
            20   25   30

Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met Leu Asp Phe Arg Leu
        35   40   45

Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser Thr Glu Lys Leu Glu
    50   55   60

Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser Thr Asp Asp Lys Leu
65   70   75   80

Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr Glu Asp Tyr Lys Gln
                85   90   95

Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile Ala Glu Lys Arg Leu
            100   105   110

Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Ile
        115   120   125

Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp Leu Ser Ile His His
    130   135   140

Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr Asp Gly Tyr Ala Lys
145   150   155   160

Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu Asn Tyr Ile Asp Gln
                165   170   175

Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys Glu Ala Ile Glu Lys
            180   185   190

Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro Tyr Thr Tyr Tyr Asn
        195   200   205

Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His Glu Glu Ala Leu Lys
    210   215   220

Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe Glu Thr Lys Ala Lys
225   230   235   240

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Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr Arg Ser Leu Phe Lys
                245                 250                 255

Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile Asp Thr Gly Phe Lys
            260                 265                 270

Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu Leu Lys Phe Lys Thr
        275                 280                 285

Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys Leu Glu Val Ile Lys
    290                 295                 300

Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala Trp Val Asp Leu Glu
305                 310                 315                 320

Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg Glu Asn Lys Leu Tyr
                325                 330                 335

Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp Lys Ala Ser Lys Leu
            340                 345                 350

Ala Gly Arg Gly Gly Glu
        355

<210>  35
<211>  2101
<212>  DNA
<213>  Bacillus licheniformis

<220>
<221>  CDS
<222>  (501)..(1598)

<400>  35
aaaacagcat gggctaaaat gacgctggac aaagcagtgt ccttaggctt ggaggcaaat      60

gcatatttga aaagaaacac agacggaaaa gaactgagct gcagcccggc tggaggaaaa     120

ggaaaagtgc tcccggggca gacatcctgt tatacaccga tggttgattt cgatccgcgt     180

tcttcatatg cgatgtagaa acattatcaa tccattaaca ggagctctca cttattccta     240

tacaagttcg tattcatatt tgaagaagta gtgtataaaa gcaccctttc agcaagggtg     300

ctttttgctg tcttatcagt cacggtttca cagctattga agagtcattt gacctaataa     360

aagagtggga aaagtggggg attcaggaaa ctgtgtaaaa tgaactatta ctattaattt     420

atacagggag gaaaatatag tatgatatga ataatgaata aaatacaaaa aaattgaata     480

tcggaagaaa ggagctccat atg aac aag atc gcc gcg gaa gaa gtc gcc aac    533
                      Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn
                      1               5                   10

atc ctt aat aca tgg tac cgc gcc atc aga aga aat gat gct gaa cag      581
Ile Leu Asn Thr Trp Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln
            15                  20                  25
```

10295.204.ST25.txt

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tcg atc cga ata ttt gaa gaa gtc aaa ccg atg ctg gca gag atg gag      629
Ser Ile Arg Ile Phe Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu
        30                  35                  40

gaa gac caa gag gtt tta atc tac tat tct ctg ctg gaa ctg cgg cat      677
Glu Asp Gln Glu Val Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His
    45                  50                  55

aaa atc atg ctg tat gat acg cgg gga aaa aag ata gaa cag caa gag      725
Lys Ile Met Leu Tyr Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu
60                  65                  70                  75

gag tta acg aac ggc ggc agt gct gca tca cat atg aca tcc tat tac      773
Glu Leu Thr Asn Gly Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr
                80                  85                  90

tac tac ctg ttt tca gga gct tat gaa gtg tat aaa aag aat tat gag      821
Tyr Tyr Leu Phe Ser Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu
            95                  100                 105

cag gcg atc agc ttc tat aaa att gcc gag aag aag ctt gct cat gta      869
Gln Ala Ile Ser Phe Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val
        110                 115                 120

cat gat gaa att gag gtg gcg caa ttt cac gat aaa gtc gga aag ctc      917
His Asp Glu Ile Glu Val Ala Gln Phe His Asp Lys Val Gly Lys Leu
    125                 130                 135

tac tat tac ttg ggc cag aat atc gtc tct tta aac cat acc cgg cag      965
Tyr Tyr Tyr Leu Gly Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln
140                 145                 150                 155

gcg atg gaa att ttc aag ggg cat ggc gac cat gat atg aac ctt gtt      1013
Ala Met Glu Ile Phe Lys Gly His Gly Asp His Asp Met Asn Leu Val
                160                 165                 170

tcc act tat att acg atg gcc gga aat tat aca gag atg ggg aaa tat      1061
Ser Thr Tyr Ile Thr Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr
            175                 180                 185

aca gag gcg gaa gaa tat tta aca gaa gcc atc cat acg gta aga aaa      1109
Thr Glu Ala Glu Glu Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys
        190                 195                 200

gcc ggc gac tgt ttt aaa gaa atg cag ctc ctt cat aat ttt gcc ttg      1157
Ala Gly Asp Cys Phe Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu
    205                 210                 215

ctt tat gcg gcg atg gac aat tcg gaa aaa agc att cag ttt tta gaa      1205
Leu Tyr Ala Ala Met Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu
220                 225                 230                 235

atc gtt ttg gat gat caa gca tat gct gca tca gat tat tat ttc aat      1253
Ile Val Leu Asp Asp Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn
                240                 245                 250

gct gtg ttt tta atg atc aaa gag ctg ttt aaa gtc gga gac cat aaa      1301
Ala Val Phe Leu Met Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys
            255                 260                 265

cgc gct gca gcc ttt tac aaa gaa ggg aag gaa agg tcg aaa tcc gcg      1349
Arg Ala Ala Ala Phe Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala
        270                 275                 280

gcg aat aaa ata ttt gac gcc aaa atc gat att tta tat gcg gct tat      1397
Ala Asn Lys Ile Phe Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr
    285                 290                 295
```

```
gca gga gat ggt gaa cag gcg gtt aaa gac tgc aaa gac aac att gaa      1445
Ala Gly Asp Gly Glu Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu
300                 305                 310                 315

atc ctg ttt caa aca aag caa tac gac agc gcc aga gaa ctt tcg ctc      1493
Ile Leu Phe Gln Thr Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu
                320                 325                 330

tta acg gcc aat gtt tac aga tca aag tca ctt tat aaa gaa gcc gca      1541
Leu Thr Ala Asn Val Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala
            335                 340                 345

cat ttc ttt ttg gaa gcg att aaa gcg gaa gaa aaa atg aaa aaa gtg      1589
His Phe Phe Leu Glu Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val
        350                 355                 360

gag gga atg tgatgaaaaa actgttcatt gttgctgcga ttgctgccgt              1638
Glu Gly Met
    365

cgtatgttcg ggatggtttg cggcagaaac tcactgggca tccggcgaca tgcaggttgc    1698

tgaaaagatg gtcggttaaa tcgaatactc ggaacaaata tgaacatccg ctcctgagca    1758

tcagggcgga tttttttggg aaggtaaagt aaattaaggc ataagaaacg cggttagaca    1818

atgaacactt cttcaccact atttagggtg gtcaacctaa acaaaggtac gaaacctgtg    1878

ctgactactt ttactccgat gtcctttcag ctattcttgt cagtaagatc attccccatc    1938

tcttcaacgc ctcaggcatc acctattaaa aaaatcataa ttgaaacttg tcagcaaata    1998

tgttgcataa cacgaggatg tttccacaat aattaaacat taagactttt ttgacttcca    2058

gaaggaagaa caagatattt atgtaaaatc actcttttat tca                      2101
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<210> 36
<211> 366
<212> PRT
<213> Bacillus licheniformis

<400> 36

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Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn Ile Leu Asn Thr Trp
1               5                   10                  15

Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln Ser Ile Arg Ile Phe
            20                  25                  30

Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu Glu Asp Gln Glu Val
        35                  40                  45

Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His Lys Ile Met Leu Tyr
    50                  55                  60

Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu Glu Leu Thr Asn Gly
65                  70                  75                  80

Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr Tyr Tyr Leu Phe Ser
                85                  90                  95
```

Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu Gln Ala Ile Ser Phe
100 105 110

Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val His Asp Glu Ile Glu
115 120 125

Val Ala Gln Phe His Asp Lys Val Gly Lys Leu Tyr Tyr Tyr Leu Gly
130 135 140

Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln Ala Met Glu Ile Phe
145 150 155 160

Lys Gly His Gly Asp His Asp Met Asn Leu Val Ser Thr Tyr Ile Thr
165 170 175

Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr Thr Glu Ala Glu Glu
180 185 190

Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys Ala Gly Asp Cys Phe
195 200 205

Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu Leu Tyr Ala Ala Met
210 215 220

Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu Ile Val Leu Asp Asp
225 230 235 240

Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn Ala Val Phe Leu Met
245 250 255

Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys Arg Ala Ala Ala Phe
260 265 270

Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala Ala Asn Lys Ile Phe
275 280 285

Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr Ala Gly Asp Gly Glu
290 295 300

Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu Ile Leu Phe Gln Thr
305 310 315 320

Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu Leu Thr Ala Asn Val
325 330 335

Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala His Phe Phe Leu Glu
340 345 350

Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val Glu Gly Met
355 360 365

10295.204.ST25.txt

<210> 37
<211> 1936
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (384)..(1433)

<400> 37
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catcattcaa gaacatcctg ataaacaaat cgaatccctt aaccctgata tgtgtccttg     120

tttgacaatg aacagaatcg acatgccgca tttgctgtgg tcgctggagc agatcgacaa     180

aggtgaaccg acaggcgtga tcaaagtgga tcaagatatt gcaaaagatg ccattcttgc     240

gctgaatcgg atgttaacga tccgttaact ttttggagaa caagttttta tcataacccc     300

tccgctatgc gcataaattt gtggagaagc atatttgtta ttctcatctg ttcgttcacg     360

tttttgcata ggaggggaaa acg ttg aaa att cat att gtc caa aag ggc gat     413
                          Leu Lys Ile His Ile Val Gln Lys Gly Asp
                          1               5                   10

tct ctg gaa aaa atc gcg gaa aga tat gaa gtg gac ttt gaa gaa ctg       461
Ser Leu Glu Lys Ile Ala Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu
                15                  20                  25

aaa aag ctg aat tcg cag ctg agc aat cca gac ttg atc atg ccg ggc       509
Lys Lys Leu Asn Ser Gln Leu Ser Asn Pro Asp Leu Ile Met Pro Gly
            30                  35                  40

atg aaa atc aaa gta ccg tca ggg gga gtg ccg gtc aaa aaa gaa gaa       557
Met Lys Ile Lys Val Pro Ser Gly Gly Val Pro Val Lys Lys Glu Glu
        45                  50                  55

cag ctc aat atg cga aag gaa tta ccg aaa aaa cag cag gaa cat cca       605
Gln Leu Asn Met Arg Lys Glu Leu Pro Lys Lys Gln Gln Glu His Pro
    60                  65                  70

ttt gca aaa gaa aag ccg aaa agc aag ctt gat gtt gaa gat ata aaa       653
Phe Ala Lys Glu Lys Pro Lys Ser Lys Leu Asp Val Glu Asp Ile Lys
75                  80                  85                  90

ccg aaa gaa aag cct tcg gtt cct tat gtt ccg cct gtc ccg aac atc       701
Pro Lys Glu Lys Pro Ser Val Pro Tyr Val Pro Pro Val Pro Asn Ile
                95                  100                 105

gga caa tca agt ttg cct gaa ggc gac att tcg aat ttg tat caa agc       749
Gly Gln Ser Ser Leu Pro Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser
            110                 115                 120

gtc aat cag ctt cat cag ccg tac gta cct cca aaa cct tat gaa cat       797
Val Asn Gln Leu His Gln Pro Tyr Val Pro Pro Lys Pro Tyr Glu His
        125                 130                 135

caa gag aaa ggc ccc aac atg tat aat cca tgg aca aat gag gag gaa       845
Gln Glu Lys Gly Pro Asn Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu
    140                 145                 150

aac cat atg gaa aat gtc aat tat ccg aat gtt ccg cag ccg cca aat       893
Asn His Met Glu Asn Val Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn
155                 160                 165                 170

gtc ggt gca gca ggt gat gaa aat aag cag ttt cac ggc atg ccg aat       941
```

Val Gly Ala Ala Gly Asp Glu Asn Lys Gln Phe His Gly Met Pro Asn
175 180 185

gta gct gca gcg gga tat cat cac cat cca tat cct tat ccg ttc tat 989
Val Ala Ala Ala Gly Tyr His His His Pro Tyr Pro Tyr Pro Phe Tyr
190 195 200

cct gga ggc tgc tgg att cct gtt tca ccg gtg ctg cct gga tcg gga 1037
Pro Gly Gly Cys Trp Ile Pro Val Ser Pro Val Leu Pro Gly Ser Gly
205 210 215

ttg tgc cat cct tgg tat cca tat cct gct caa atg cct tat atg cat 1085
Leu Cys His Pro Trp Tyr Pro Tyr Pro Ala Gln Met Pro Tyr Met His
220 225 230

cag cct agc tat gta tct cct gct gaa tat gac gat gat gac aac atg 1133
Gln Pro Ser Tyr Val Ser Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met
235 240 245 250

ggg cat gac aat gcc ggt cat cac gga tac cat cat cag ccg atg act 1181
Gly His Asp Asn Ala Gly His His Gly Tyr His His Gln Pro Met Thr
255 260 265

gcc ccg gca tat gcg cct tac cag ccg ttc ccg gga ttt gca ccg cca 1229
Ala Pro Ala Tyr Ala Pro Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro
270 275 280

aac gtc ggt cac gcc ggg gac cct aat atg gca cac ggc aaa gaa gat 1277
Asn Val Gly His Ala Gly Asp Pro Asn Met Ala His Gly Lys Glu Asp
285 290 295

gac tgc ggg tgc ggg ccg ggc caa ttc ccg gga ggt ttt cca ggt gcg 1325
Asp Cys Gly Cys Gly Pro Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala
300 305 310

gcg cca tat gga cag atg ccg caa atg gga gct ccg tac ggt atg ggg 1373
Ala Pro Tyr Gly Gln Met Pro Gln Met Gly Ala Pro Tyr Gly Met Gly
315 320 325 330

gga tac gga cag cag cct gca ggg gga cag atg ttt aac aga ccg gaa 1421
Gly Tyr Gly Gln Gln Pro Ala Gly Gly Gln Met Phe Asn Arg Pro Glu
335 340 345

gat gat gaa gac tgattcggaa tgggacgatg atctatcgtt cctttttat 1473
Asp Asp Glu Asp
350

tgtggaccgc tataaacatt ttcatgctat ttaacgggaa tgtctataac tgtcaagggt 1533
aactcttcgc atcccgcaca tcctaaaaaa gagcgcaatg ctcaaattca gcggttttca 1593
cggggggtac taccattgga cagcaagctg aaagtgtttt cggggatttt gcttttgaca 1653
gcaggtctat ctgcatgcgg aacgaacgac gctatagata atggaaacaa tacgcgcccg 1713
atcggatatt atctcaaatg atgcagatcg taatgcaggg tcttgataat gacggccctg 1773
ttacagaaat gcttgaaaac atgaacggga gacacggtgc aacaaacgta aacaatcgag 1833
cgggaaacgg caatcccgtt ccaacaggcg atggaactta cagccgggga gacatgaatt 1893
atcacaacca tttggtgaat acggcggata caggctatga cag 1936

<210> 38
<211> 350
<212> PRT
<213> Bacillus licheniformis

<400> 38

Leu Lys Ile His Ile Val Gln Lys Gly Asp Ser Leu Glu Lys Ile Ala
1 5 10 15

Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu Lys Lys Leu Asn Ser Gln
20 25 30

Leu Ser Asn Pro Asp Leu Ile Met Pro Gly Met Lys Ile Lys Val Pro
35 40 45

Ser Gly Gly Val Pro Val Lys Lys Glu Glu Gln Leu Asn Met Arg Lys
50 55 60

Glu Leu Pro Lys Lys Gln Gln Glu His Pro Phe Ala Lys Glu Lys Pro
65 70 75 80

Lys Ser Lys Leu Asp Val Glu Asp Ile Lys Pro Lys Glu Lys Pro Ser
85 90 95

Val Pro Tyr Val Pro Pro Val Pro Asn Ile Gly Gln Ser Ser Leu Pro
100 105 110

Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser Val Asn Gln Leu His Gln
115 120 125

Pro Tyr Val Pro Pro Lys Pro Tyr Glu His Gln Glu Lys Gly Pro Asn
130 135 140

Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu Asn His Met Glu Asn Val
145 150 155 160

Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn Val Gly Ala Ala Gly Asp
165 170 175

Glu Asn Lys Gln Phe His Gly Met Pro Asn Val Ala Ala Ala Gly Tyr
180 185 190

His His His Pro Tyr Pro Tyr Pro Phe Tyr Pro Gly Gly Cys Trp Ile
195 200 205

Pro Val Ser Pro Val Leu Pro Gly Ser Gly Leu Cys His Pro Trp Tyr
210 215 220

Pro Tyr Pro Ala Gln Met Pro Tyr Met His Gln Pro Ser Tyr Val Ser
225 230 235 240

Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met Gly His Asp Asn Ala Gly
245 250 255

His His Gly Tyr His His Gln Pro Met Thr Ala Pro Ala Tyr Ala Pro

260 265 270

Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro Asn Val Gly His Ala Gly
275 280 285

Asp Pro Asn Met Ala His Gly Lys Glu Asp Asp Cys Gly Cys Gly Pro
290 295 300

Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala Ala Pro Tyr Gly Gln Met
305 310 315 320

Pro Gln Met Gly Ala Pro Tyr Gly Met Gly Gly Tyr Gly Gln Gln Pro
325 330 335

Ala Gly Gly Gln Met Phe Asn Arg Pro Glu Asp Asp Glu Asp
340 345 350

<210> 39
<211> 2027
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1526)

<400> 39
aagagcaaat tctgtctatg agcacaacag aagaggttgt acaattcgta aaagaaacct 60
tcaacctggc ataagcaatt gaaaatccgg accggcatca ccaatgcccg tccgggtttt 120
ttgtttatct gaatgatccc ggctgcggcg gagataatac atgtgaccaa ttgttagaaa 180
gggggattct gatatgccta ggcagccatt caaactggga gatgaggtgt atgtcattta 240
ccggaatccg catgcagcga atgtggcgca tataaaggaa gctgaagtcg ttgatcatcc 300
gcttcacgaa ggcgaactgg cattgtttat gtatgataca tatcacgcct ttgccgaaga 360
tgatgccgtt ttttcttcat atgaagaggc ggaacggctt taccgtgaat tatttgacgg 420
gatatgaaga cattaccggt atatcacatc ctctaaatgc aaaaagtaat ggaaatatgc 480
aaaggatgtg tctgtttcca atg gta aaa ccg ttt gtt ccc caa ctc gtc tat 533
Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr
1 5 10

att gaa ccg aga gcc ctg gaa tat ccg ctt gga aaa gag ctg agg gat 581
Ile Glu Pro Arg Ala Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp
15 20 25

aaa ttt tca aac atg gga ctt gag atc agg gaa aca act tca cac aac 629
Lys Phe Ser Asn Met Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn
30 35 40

cag gtg agg aat atc ccg ggg gaa ggc cac ctg caa aaa tac aga aat 677
Gln Val Arg Asn Ile Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn
45 50 55

gcg aaa tcc act ttg gtg atc ggc gtc aga aaa aca ttg aag ttc gat 725
Ala Lys Ser Thr Leu Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp

60 65 70 75

tcg tca aaa ccg tcc gca gaa tac gcg atc ccg ttt gca aca ggg tgt 773
Ser Ser Lys Pro Ser Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys
80 85 90

atg ggt cac tgt cat tac tgc tac ctg caa acg aca atg ggc agc aag 821
Met Gly His Cys His Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys
95 100 105

ccg tat atc aga acg tac gtc aat gtg gag gaa ata ctt gag cag gcg 869
Pro Tyr Ile Arg Thr Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala
110 115 120

gat caa tat ata aaa gaa agg gct ccc gaa gat acg cgg ttt gaa gct 917
Asp Gln Tyr Ile Lys Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala
125 130 135

tcc tgc aca tcc gat atc gtc gga att gac cat ttg aca cat acg tta 965
Ser Cys Thr Ser Asp Ile Val Gly Ile Asp His Leu Thr His Thr Leu
140 145 150 155

aaa cgc gcc att gag cat ttc ggt caa acc gac cat ggt aag ctg cgt 1013
Lys Arg Ala Ile Glu His Phe Gly Gln Thr Asp His Gly Lys Leu Arg
160 165 170

ttc gtg aca aaa ttt cat cat gtc gac cat ttg ctc gat gcc aag cac 1061
Phe Val Thr Lys Phe His His Val Asp His Leu Leu Asp Ala Lys His
175 180 185

aac gga aaa acg cgc ttc cgc ttc agc gtg aat gcc gaa tat gtc att 1109
Asn Gly Lys Thr Arg Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile
190 195 200

aaa agc ttt gaa ccc ggc aca tcc ccg ttg gat aaa cgg atc gaa gcc 1157
Lys Ser Phe Glu Pro Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala
205 210 215

gcc gtg aaa gta gcg gaa gcg ggc tat ccg ctc ggt ttt atc atc gct 1205
Ala Val Lys Val Ala Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala
220 225 230 235

ccg att tat att cat gac ggc tgg cag gaa ggc tac aga gtt ctg ctg 1253
Pro Ile Tyr Ile His Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu
240 245 250

gaa aag ctc gat cgt gcg ctg ccg cag cat gcg agg cgc gac atc acc 1301
Glu Lys Leu Asp Arg Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr
255 260 265

ttt gaa atg atc cag cat aga ttc acg aag ccg gca aag aga gtc att 1349
Phe Glu Met Ile Gln His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile
270 275 280

gaa aaa aac tat cca aag aca aag ctc gaa ctg gat gaa gaa aaa cgg 1397
Glu Lys Asn Tyr Pro Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg
285 290 295

cgc tat aaa tgg ggc aga tac ggg att ggc aaa tac att tat cag aag 1445
Arg Tyr Lys Trp Gly Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys
300 305 310 315

gat gaa gaa gca gag ctt cgc agc gcc ctt gaa tcg tat atc gac aac 1493
Asp Glu Glu Ala Glu Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn
320 325 330

tat ttt ccc gaa gca aaa atc gaa tat ttc aca taacagagct ttagttgata 1546
Tyr Phe Pro Glu Ala Lys Ile Glu Tyr Phe Thr

335 340

aagctctgtt ttttgttttg aaaacattat gttaaaaaag gatttttcca ctccattaac 1606

accgcataat caagcgattc ctcatcttca atgtagccgg gaatcacaca aactggagag 1666

cgtccgcaat gaagcaggaa cgagagcact ggatcgcgct tttccccgtc caatacagct 1726

tgaacatact gttcgggcgt catttcttca gccgacttgt gataatgggg aatccgtccg 1786

ccgccaatga gacgcttgag ccctttaaag accgtcagtt catacatgga ttgcatcagc 1846

cgcattccga tgccgagttt tcgatagtcg ggggacacgg aaatatcgac gacataaagg 1906

gagtttccat cgttttgatg tgtgccgata tacccgttgt ccgtcacttc atcccagctg 1966

tggtgcggat gatgcggatc aaaatcagcc atgagcgctg tcatcgaacc gatgatgcgg 2026

c 2027

<210> 40
<211> 342
<212> PRT
<213> Bacillus licheniformis

<400> 40

Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr Ile Glu Pro Arg Ala
1 5 10 15

Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp Lys Phe Ser Asn Met
20 25 30

Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn Gln Val Arg Asn Ile
35 40 45

Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn Ala Lys Ser Thr Leu
50 55 60

Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp Ser Ser Lys Pro Ser
65 70 75 80

Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys Met Gly His Cys His
85 90 95

Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys Pro Tyr Ile Arg Thr
100 105 110

Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala Asp Gln Tyr Ile Lys
115 120 125

Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala Ser Cys Thr Ser Asp
130 135 140

Ile Val Gly Ile Asp His Leu Thr His Thr Leu Lys Arg Ala Ile Glu
145 150 155 160

His Phe Gly Gln Thr Asp His Gly Lys Leu Arg Phe Val Thr Lys Phe
165 170 175

His His Val Asp His Leu Leu Asp Ala Lys His Asn Gly Lys Thr Arg
180 185 190

Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile Lys Ser Phe Glu Pro
195 200 205

Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala Ala Val Lys Val Ala
210 215 220

Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala Pro Ile Tyr Ile His
225 230 235 240

Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu Glu Lys Leu Asp Arg
245 250 255

Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr Phe Glu Met Ile Gln
260 265 270

His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile Glu Lys Asn Tyr Pro
275 280 285

Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg Arg Tyr Lys Trp Gly
290 295 300

Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys Asp Glu Glu Ala Glu
305 310 315 320

Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn Tyr Phe Pro Glu Ala
325 330 335

Lys Ile Glu Tyr Phe Thr
340

<210> 41
<211> 905
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(905)

<400> 41
acaaatacag tacaggccgg gaagacggga tatacaaggc ttgcaaagcg gacgctcgtc 60

tccatttcat cgaaagacgg aaccgatttg atcgccgtca caatcaatgc ccctgacgac 120

tggaatgatc atatgaacat gttcaactat gtattcggcc agtacaaaac atatatcatc 180

gccaaaaaag gcgagattcc gaaattaaaa gactcttttt acggacatac agcttttatt 240

aaacgggatg tcacatatct tttaaacgaa gaggaaaaag aagatgtgaa ggttgatatc 300

gagcttcttg aaccgaaaaa atcatggcgt aaaaacaaaa aagaaatccc ggacatcatc 360

ggagaaatga acgtcatgtt cgacggaaaa acgattgcaa gcgtaccgat ctattatgaa 420

aacgagcgaa acaaaaatcc gaaaaaatcg tttttcgaga cctttcaatc cgtattccaa 480

aaagcggcgg gcggttcatc atg gtc aat ata atc tgg gtc ggc tta acg gtg 533
Met Val Asn Ile Ile Trp Val Gly Leu Thr Val
1 5 10

atc ggt atg gtg ttt gcg ctt ttc aac ggc acg gtt cag gaa gtt aat 581
Ile Gly Met Val Phe Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn
15 20 25

gaa gct gta ttt aaa gga tcg aag gaa gcc gtc acg att gtg atc gga 629
Glu Ala Val Phe Lys Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly
30 35 40

ctg atg agc gtc ctt gtt ttt tgg ctg ggg gtg atg aaa atc gct gaa 677
Leu Met Ser Val Leu Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu
45 50 55

cag tcc ggg ctt ctc gaa aaa ttc agc agg ctg tgc cgg ccg ttc att 725
Gln Ser Gly Leu Leu Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile
60 65 70 75

tcg aag ctg ttt ccc gag atc cct ccg gat cat ccg gcg atg gga tat 773
Ser Lys Leu Phe Pro Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr
80 85 90

att tta tcc aat tta atg gcc aac ttt ttc gga ttg ggc aat gca gcg 821
Ile Leu Ser Asn Leu Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala
95 100 105

aca ccg ctc ggt att aaa gcg atg gaa cag atg aag gcg ctc aac cgg 869
Thr Pro Leu Gly Ile Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg
110 115 120

aac cgc agg gaa gcg agc cgc tca atg cac cca ggc 905
Asn Arg Arg Glu Ala Ser Arg Ser Met His Pro Gly
125 130 135

<210> 42
<211> 135
<212> PRT
<213> Bacillus licheniformis

<400> 42

Met Val Asn Ile Ile Trp Val Gly Leu Thr Val Ile Gly Met Val Phe
1 5 10 15

Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn Glu Ala Val Phe Lys
20 25 30

Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly Leu Met Ser Val Leu
35 40 45

Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu Gln Ser Gly Leu Leu
50 55 60

Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile Ser Lys Leu Phe Pro

65 70 75 80

Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr Ile Leu Ser Asn Leu
85 90 95

Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala Thr Pro Leu Gly Ile
100 105 110

Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg Asn Arg Arg Glu Ala
115 120 125

Ser Arg Ser Met His Pro Gly
130 135

<210> 43
<211> 1568
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1076)

<220>
<221> CDS
<222> (1112)..(1567)

<400> 43
gattagatct tcagtttttt gcatctaaaa aaggagtagg ttcaacgaaa aacggacgtg 60

actctgaagc gaagcgccta ggtgctaaac gtgcagacgg tcaattcgta tctggccgtt 120

caatccttta tcgtcagcgc ggaacaaaaa tctatccaag tgaaaacgtt gggcgcggcc 180

gatattacac tctatttgca aaagtcgacg gaactgttaa attcgaacct ttcggccgta 240

cccccaaaaa agtgagcgta tatcctgtag cctaaccttt aaacgaaact ccggtcgttc 300

tgaccggagt tttttacatt cagcaccatg acttgcttaa aacaccttcc cgacgcctaa 360

ataaggccgg gtttccgctc tgattctgct tcgttaaagt atataaacgt gtttcattta 420

tactgccttc tctgttataa ttcaaagtac aaactgaatc agactcctaa aagagagacc 480

aaacgattgg gagtgccaaa atg gaa gaa act tcg aaa aaa cga gaa aag aat 533
Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn
1 5 10

atg gac gat aag gct ttg acc cat gag ctt atc cat ctg ctc agc cac 581
Met Asp Asp Lys Ala Leu Thr His Glu Leu Ile His Leu Leu Ser His
15 20 25

tca agg cac gac tgg atg aat aaa ctg caa ttg att aaa gga aac tta 629
Ser Arg His Asp Trp Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu
30 35 40

aca tta aaa aag tat gac cgc gta ttt gaa att atc gat gaa gtg gtc 677
Thr Leu Lys Lys Tyr Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val
45 50 55

atc gaa gct cag cat gaa tca aag ctt tca aac ctt aga atc ccg cgc 725
Ile Glu Ala Gln His Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg

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                                                              70              75
60                     65
gcg gcg tat gag ctg ctt aca ttt aac tgg atg gcc cat tcg ctg acg      773
Ala Ala Tyr Glu Leu Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr
                80                      85                  90

ctt gaa tat gag gtg atc ggt caa gtc aag gat ttg tca gct tat gaa      821
Leu Glu Tyr Glu Val Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu
            95                      100                 105

gaa agg ctc gtc gtt ctc atc aga aag ctg ttt ggg att ttt gac gat      869
Glu Arg Leu Val Val Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp
        110                     115                 120

gcc gtt ttg aaa ggc agc gac aat cat ctg acg atc acg ctg cag acg      917
Ala Val Leu Lys Gly Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr
    125                     130                 135

gac ggt ccg gac gac cgc ctc gtc atc ttt ctc gat ttc cac ggc gta      965
Asp Gly Pro Asp Asp Arg Leu Val Ile Phe Leu Asp Phe His Gly Val
140                     145                 150                 155

ttc aca aag ctg acc ggt atc aaa gac ttt cat cat tca ctg gcc gac      1013
Phe Thr Lys Leu Thr Gly Ile Lys Asp Phe His His Ser Leu Ala Asp
                160                     165                 170

ttt tat gaa atc aag cgg ttt gat gta aca gac cgt gag tgc atc gcc      1061
Phe Tyr Glu Ile Lys Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala
            175                     180                 185

gaa att cat atc aag taaagcggtt ttttaggaat agaacggagg acatt atg      1114
Glu Ile His Ile Lys                                           Met
        190

ttt gtt gat cag gtg aaa ata tac gta aaa ggc gga gac gga ggc aac      1162
Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly Asn
    195                     200                 205

ggt atg gtt gct ttc cgc cgc gaa aaa tat gtg cca aaa gga ggc cct      1210
Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly Pro
210                     215                 220                 225

gcc gga ggt gac ggc gga aaa ggc gga gac gtc gtt ttc aaa gtt gac      1258
Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val Asp
                230                     235                 240

gaa ggt ctc agc acg ctg atg gat ttt aga tat caa aga cat ttt aag      1306
Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe Lys
            245                     250                 255

gca gcg cgc gga gaa cac ggc atg tct aaa aac cag cac ggc cga aat      1354
Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg Asn
        260                     265                 270

gcc gaa gac atg gtt gtg aaa gtc ccg ccc ggc acg gtt gtc att gac      1402
Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile Asp
    275                     280                 285

gat gat aca aaa cag gtc atc gct gat tta acg gag cac gga cag gaa      1450
Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln Glu
290                     295                 300                 305

gcc gtc atc gca aaa ggg gga cgc ggc gga cgg ggc aat aca cgt ttt      1498
Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg Phe
                310                     315                 320

gcg acg cct gcc aac ccg gcg ccg cag ctt tct gaa aac ggc gaa ccc      1546
Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu Pro
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325 330 335

ggc aag gag cgc tat att gtt c 1568
Gly Lys Glu Arg Tyr Ile Val
340

<210> 44
<211> 192
<212> PRT
<213> Bacillus licheniformis

<400> 44

Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn Met Asp Asp Lys Ala
1 5 10 15

Leu Thr His Glu Leu Ile His Leu Leu Ser His Ser Arg His Asp Trp
20 25 30

Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu Thr Leu Lys Lys Tyr
35 40 45

Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val Ile Glu Ala Gln His
50 55 60

Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg Ala Ala Tyr Glu Leu
65 70 75 80

Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr Leu Glu Tyr Glu Val
85 90 95

Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu Glu Arg Leu Val Val
100 105 110

Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp Ala Val Leu Lys Gly
115 120 125

Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr Asp Gly Pro Asp Asp
130 135 140

Arg Leu Val Ile Phe Leu Asp Phe His Gly Val Phe Thr Lys Leu Thr
145 150 155 160

Gly Ile Lys Asp Phe His His Ser Leu Ala Asp Phe Tyr Glu Ile Lys
165 170 175

Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala Glu Ile His Ile Lys
180 185 190

<210> 45
<211> 152
<212> PRT
<213> Bacillus licheniformis

<400> 45

Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
1 5 10 15

Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
35 40 45

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
50 55 60

Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
65 70 75 80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
85 90 95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
100 105 110

Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
115 120 125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
130 135 140

Pro Gly Lys Glu Arg Tyr Ile Val
145 150

<210> 46
<211> 1849
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1346)

<400> 46
tcctgcaacg atccagcttg cgggggcgga aattgaactt gttccgacca tctcccgaga 60
agtccggctg aaaagggctt tggaatcggt caaacaaaac tatgatttca tgattattga 120
ctgcccgccg tcattagggc tgcttacaat caatgcgctt acggcttccg attccgtcgt 180
gattccggtc cagtgcgagt attatgcgct ggaagggctg agccagctgc tcaactctgt 240
ccggctcgtg caaaaacatt taaatacgga tctgatgatc gacggcgtat tgctgacaat 300
gcttgatgca agaacgaatt taggcataca ggtcatcgaa gaagtgaaaa agtacttccg 360
cgataaagta tacaaaacgg ttatcccccg gaatgtccgg ctcagtgaag cgccgagtca 420
tggaaagccg atcattttat atgatccccg ttccagagga gcggaagtct atttagaatt 480

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agcaaaggaa gtggctgcga atg cct aaa ggt ctc gga aaa ggg att aat gca     533
                      Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala
                      1               5                   10

ttg ttt tca aat gtt gat tta tcc gaa gaa acg gtt gag gaa atc aag       581
Leu Phe Ser Asn Val Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys
            15                  20                  25

ctg caa gac ttg cgg ccc aac cct tat cag cca aga aaa acg ttt gat       629
Leu Gln Asp Leu Arg Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp
        30                  35                  40

gac caa tcg tta aaa gat ttg aag gag tcc att ttg cag cac ggt gtt       677
Asp Gln Ser Leu Lys Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val
    45                  50                  55

ttg cag ccc atc atc gtc aga aag tca att aaa ggc tat gac att gtg       725
Leu Gln Pro Ile Ile Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val
60                  65                  70                  75

gcc gga gaa cgc cgt ttc cgg gct gct gaa aag gcc gga ttg gaa acc       773
Ala Gly Glu Arg Arg Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr
                80                  85                  90

att cct gcg att gtg cgc gag ctg tcg gaa tcc ctg atg atg gag att       821
Ile Pro Ala Ile Val Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile
            95                  100                 105

gcc cta ttg gaa aat ctt caa cga gaa gac ctg tct ccg ctt gaa gaa       869
Ala Leu Leu Glu Asn Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu
        110                 115                 120

gca aaa gcc tat gaa tct ttg ctc aaa cat ctc gat atg acc cag gaa       917
Ala Lys Ala Tyr Glu Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu
    125                 130                 135

cag ctg gcg aaa agg ctt gga aaa agc agg cct cac atc gcc aac cac       965
Gln Leu Ala Lys Arg Leu Gly Lys Ser Arg Pro His Ile Ala Asn His
140                 145                 150                 155

ttg cgg ctg ctg aca ctt cct gaa gac gtt caa aag tta atc gac aac      1013
Leu Arg Leu Leu Thr Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn
                160                 165                 170

ggc acg tta tcg atg ggc cat ggc cga aca ttg ctt gga ttg aaa aac      1061
Gly Thr Leu Ser Met Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn
            175                 180                 185

aag aaa aag ctt gag ccg ctt gtt caa aag gtc gtg tcc gaa cag ttg      1109
Lys Lys Lys Leu Glu Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu
        190                 195                 200

aac gtc cgc cag ttg gaa aag tta att caa cag ttg aac gct gat gtt      1157
Asn Val Arg Gln Leu Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val
    205                 210                 215

cca cgt gaa aca aag aag ccg aaa caa gtc aaa gat gca gtg atc aag      1205
Pro Arg Glu Thr Lys Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys
220                 225                 230                 235

gaa cgg gaa tcg tat ttg cga aac tat ttt gga aca ccg gtg acc att      1253
Glu Arg Glu Ser Tyr Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile
                240                 245                 250

aaa aag caa aag aaa aaa ggc agg atc gaa atc gaa ttc tac tca aat      1301
Lys Lys Gln Lys Lys Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn
            255                 260                 265
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gaa gac ttg gag cgt att ctc gaa tta ttg gct caa gaa gac gca 1346
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270 275 280

taagcttaaa aaccatctga tcatgtacag atggtttttt tatgacattc ttccggtcat 1406

tctttcaatt ggtgacacat ggcgccgctg cgatccggtc ttttccagat gcgacagccc 1466

gtccgcaagc acatttgcca tgctcatgac aagattgagc cttgtatttt gcaggacaaa 1526

atactccata aaaccgctga cattgacaat tccgttaata tgcacgtggc cgacttccgg 1586

caaacttttc tgaacgcctg ctcccggctt caaaggccct ttgccgattt ggaaagaccc 1646

cacgcttttg gttcgtccaa gacaggcgtc gatcgcgatc ataaaaggat tttgatgctg 1706

ctgatgaata tgatcaagct tttcatttaa gttcacggcg tgaaccgggt cggcaagcgt 1766

tccatagaca tgaaaacgtg tcagctgctt tgcggagagt ttcattccta cgaggggacc 1826

gagcgaatct ccggtcgagc ggt 1849

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35 40 45

Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val Leu Gln Pro Ile Ile
50 55 60

Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val Ala Gly Glu Arg Arg
65 70 75 80

Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr Ile Pro Ala Ile Val
85 90 95

Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile Ala Leu Leu Glu Asn
100 105 110

Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu Ala Lys Ala Tyr Glu
115 120 125

Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu Gln Leu Ala Lys Arg
130 135 140

Leu Gly Lys Ser Arg Pro His Ile Ala Asn His Leu Arg Leu Leu Thr
145 150 155 160

Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn Gly Thr Leu Ser Met
165 170 175

Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn Lys Lys Lys Leu Glu
180 185 190

Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu Asn Val Arg Gln Leu
195 200 205

Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val Pro Arg Glu Thr Lys
210 215 220

Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr
225 230 235 240

Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile Lys Lys Gln Lys Lys
245 250 255

Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn Glu Asp Leu Glu Arg
260 265 270

Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
275 280

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agaaatcaac aacatggcgg tgtagctcag ctggctagag cgtacggttc atacccgtga 180

ggtcgggggt tcgatcccct ccgccgctac ttatatgaag gcccgttggt caagtggtta 240

agacaccgcc ctttcacggc ggtaacacgg gttcgaatcc cgtacgggtc attccggaaa 300

ccggcttctt ctgaagccgg tttttgctg cataaaaata tgcaaaataa cgggaatgga 360

ctcgacttat caagagtgat tgaagcatgc tacaaaaagc gtcgaacagt tctttgaatt 420

cgttaccttc ttttgacaaa atcctatttc atctttcgct ataatggcaa gcaacgaata 480

aacgagtggg agatgagagc atg gaa aaa gcg gaa aga aga gtg aac agc cca 533
Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro
1 5 10

ata gct gga cct gct gtt caa aaa ttg tat tca tgg ttt ggc agc atg 581
Ile Ala Gly Pro Ala Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met
15 20 25

acg aag ctt atg atg cag cat tta tat tcc ctc ttt ttt tat aaa ggg 629
Thr Lys Leu Met Met Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly
30 35 40

ctg atc tat atg gtc atc ggt ttt tta ttg gga cga gcc ttc att ctg 677
Leu Ile Tyr Met Val Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu
45 50 55

tca gag gtc att ccc ttt gct ctt cca ttt ttc gga gcg atg ctt tta 725
Ser Glu Val Ile Pro Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu
60 65 70 75

atc aaa aaa gat aaa gct ttc ctt gca tgc ctg gcg ctt ctt gcc gga 773
Ile Lys Lys Asp Lys Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly
80 85 90

gct ctg agc ata tcg cct cag cat tcg ctg ttc gtg ctt gcg gct ctg 821
Ala Leu Ser Ile Ser Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu
95 100 105

ttt gca ttt gcg ata tgt tca aaa atg acg tcc ctt att ata aaa gac 869
Phe Ala Phe Ala Ile Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp
110 115 120

cgt gtc aga acg ctg cct gtc gtc gtc ttt ttg gcg atg gct gtg aca 917
Arg Val Arg Thr Leu Pro Val Val Val Phe Leu Ala Met Ala Val Thr
125 130 135

aga tgc gga ttc gta tat gcc gaa tac gga acg gtt tca ggt tat cac 965
Arg Cys Gly Phe Val Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His
140 145 150 155

tat att atg gct ttc gtt gaa gcc gga tta tcg ttt atc ctc aca ttg 1013
Tyr Ile Met Ala Phe Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu
160 165 170

att ttt ctg caa agc ctg ccg att gtc aca tca aag cgg gcg aaa cag 1061
Ile Phe Leu Gln Ser Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln
175 180 185

tcg ctg aaa att gaa gag atc att tgt ttt atg att tta atc gct tcc 1109
Ser Leu Lys Ile Glu Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser
190 195 200

gtt ctc acg ggc ttg aca ggc gtt tca ttt caa ggc atg cag gct gaa 1157
Val Leu Thr Gly Leu Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu
205 210 215

ctg ata ttg gcc cgt tat gtc gtg ctc gct ttc gcg ttc atc gga ggc 1205
Leu Ile Leu Ala Arg Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly
220 225 230 235

gca agc atc ggc tgt aca gtc ggg gtt gtg acc ggg ctg att ctc agc 1253
Ala Ser Ile Gly Cys Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser
240 245 250

ctc tca aac atc ggc aat tta tat cag atg agc ctg ctg gct ttc tca 1301
Leu Ser Asn Ile Gly Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser
255 260 265

ggc ctt ctc ggc ggt ttg cta aaa gaa gga aaa aag ttc ggc gca gcg 1349
Gly Leu Leu Gly Gly Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala
270 275 280

gtc ggc tta ttg att gga tct cta ttg att tct ctg tac gga gaa ggt 1397
Val Gly Leu Leu Ile Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly
285 290 295

tcg gct gaa tta gtg ccg acg ctt tat gaa tct ctg att gca atc ggc 1445
Ser Ala Glu Leu Val Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly
300 305 310 315

ctg ttc ctt tta acc cct cag tcg att acg aaa aaa gtg gcc aag tat 1493
Leu Phe Leu Leu Thr Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr
320 325 330

ata cct gga acg act gag cac gcc cag gaa cag cag cag tat gca agg 1541
Ile Pro Gly Thr Thr Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg
335 340 345

aaa atc cgc gat gtc acc gcc caa aaa gtc gat cag ttt tcg aac gtt 1589
Lys Ile Arg Asp Val Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val
350 355 360

ttt cac gct tta tcc gaa agc ttc gct acc ttt tat cat tca gct ccg 1637
Phe His Ala Leu Ser Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro
365 370 375

gac gat gaa gga aaa gaa aaa gag atc gat ctg ttt ttg agc acg gtg 1685
Asp Asp Glu Gly Lys Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val
380 385 390 395

aca gaa cat tcc tgt cag tca tgc tat aag aaa aac aag tgc tgg gtt 1733
Thr Glu His Ser Cys Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val
400 405 410

cag aac ttt gat aaa aca tat gat ttg atg aaa cgg gtt atg cag gaa 1781
Gln Asn Phe Asp Lys Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu
415 420 425

acg gaa gaa aag caa tat ttt aaa aac cgc aag ctg aaa aag gag ttt 1829
Thr Glu Glu Lys Gln Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe
430 435 440

cat cag cac tgc tcc aaa tca aag caa gta gaa gcg ctg att gaa gac 1877
His Gln His Cys Ser Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp
445 450 455

gag ctg act cat ttt agg gcg aac cag aca tta aaa caa aag gtg cat 1925
Glu Leu Thr His Phe Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His
460 465 470 475

gac agc aga cgt ctc gtt gca gag cag ctt ctc ggc gtt tct cag gtt 1973
Asp Ser Arg Arg Leu Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val
480 485 490

atg gcg gac ttt tct cgg gaa ata aaa agg gaa agg gag cag cat ttt 2021
Met Ala Asp Phe Ser Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe
495 500 505

att caa gaa gag caa att cgg gat gcg ctg cag cac ttc ggc atc gag 2069
Ile Gln Glu Glu Gln Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu
510 515 520

att cag caa gtc gaa ata tac agc ctt gag cag gga aac atc gat att 2117
Ile Gln Gln Val Glu Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile
525 530 535

gaa atg agt atc ccg tat tgc aac ggc cat gga gag tgt gaa aaa atc 2165
Glu Met Ser Ile Pro Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile
540 545 550 555

atc gct ccg atg ctg tcc gat att ttg gaa gaa caa att atc gtc aaa 2213
Ile Ala Pro Met Leu Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys
560 565 570

gca gaa cag tgc gcc ggc cat ccg aat gga tat tgt cat gtt gcc ttc 2261
Ala Glu Gln Cys Ala Gly His Pro Asn Gly Tyr Cys His Val Ala Phe
575 580 585

ggt tcg gcg aag tca tac agg gtg gtg aca gga gcc gcg cat gca gca 2309
Gly Ser Ala Lys Ser Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala
590 595 600

aaa ggc gga ggg ctt gtc tcc ggc gac agc tac aat atg atg gag ctc 2357
Lys Gly Gly Gly Leu Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu
605 610 615

ggc acc ggc aaa tat gcc gcc gcc att agc gat ggt atg gga aat ggc 2405
Gly Thr Gly Lys Tyr Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly
620 625 630 635

gca agg gcc cat ttt gaa agc aat gag acg atc aag ctg ctg gaa aag 2453
Ala Arg Ala His Phe Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys
640 645 650

att ctt cag tcg ggc atc gac gaa aaa gtg gcg att aaa acg att aac 2501
Ile Leu Gln Ser Gly Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn
655 660 665

agc att ctt tca tta agg aca aca gat gaa att tat tcg aca ttg gat 2549
Ser Ile Leu Ser Leu Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp
670 675 680

tta tcg gtc atc gat ctt cag gat gcg agc tgc aag ttt ttg aaa atc 2597
Leu Ser Val Ile Asp Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile
685 690 695

ggc tcc acc ccg agc ttt att aaa aga ggc gat caa att ata aaa gtg 2645
Gly Ser Thr Pro Ser Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val
700 705 710 715

cag gcc agc aat ctg ccg atc ggc atc att aca gaa ttc gat gtc gat 2693
Gln Ala Ser Asn Leu Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp
720 725 730

gtt gtc agc gag caa tta aaa gcg gga gac ctt ttg atc atg atg agc 2741
Val Val Ser Glu Gln Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser
735 740 745

gac gga atc ttt gaa ggg ccg aga cat gtg gaa aat cat gat ctg tgg 2789
Asp Gly Ile Phe Glu Gly Pro Arg His Val Glu Asn His Asp Leu Trp
750 755 760

atg aag cgc aaa ttg aaa tcg ctg aaa acc gag gag ccg cag gaa atc 2837
Met Lys Arg Lys Leu Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile
765 770 775

gcc gac tta atc atg gaa gaa gtg atc cgg aca agg tcg ggt ctg att 2885
Ala Asp Leu Ile Met Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile
780 785 790 795

gag gac gac atg acg gtg att gtc atc aag ctg gac cat aat acg cca 2933
Glu Asp Asp Met Thr Val Ile Val Ile Lys Leu Asp His Asn Thr Pro
800 805 810

aag tgg gcc tcc att ccg gcg ccg gct ttt ttc caa aag aat caa gag 2981
Lys Trp Ala Ser Ile Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu
815 820 825

att tct tagcattcgt ataaatcaaa tttcttctgg cgatgatgga actaaatcaa 3037
Ile Ser

gatatctttg tccaggagga ataaaaacga tgaaaaaggg gcatttgaat caaatcctgc 3097

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aggcgatgaa agaagtcgaa gggatcgctc tcgcaggcgg aggagttcac caggtggttt 3277

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Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly Leu Ile Tyr Met Val
35 40 45

Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu Ser Glu Val Ile Pro
50 55 60

Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu Ile Lys Lys Asp Lys
65 70 75 80

Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly Ala Leu Ser Ile Ser
85 90 95

Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu Phe Ala Phe Ala Ile
100 105 110

Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp Arg Val Arg Thr Leu
115 120 125

Pro Val Val Val Phe Leu Ala Met Ala Val Thr Arg Cys Gly Phe Val
130 135 140

Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His Tyr Ile Met Ala Phe
145 150 155 160

Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu Ile Phe Leu Gln Ser
165 170 175

Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln Ser Leu Lys Ile Glu
180 185 190

Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser Val Leu Thr Gly Leu
195 200 205

Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu Leu Ile Leu Ala Arg
210 215 220

Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly Ala Ser Ile Gly Cys
225 230 235 240

Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser Leu Ser Asn Ile Gly
245 250 255

Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser Gly Leu Leu Gly Gly
260 265 270

Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala Val Gly Leu Leu Ile
275 280 285

Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly Ser Ala Glu Leu Val
290 295 300

Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly Leu Phe Leu Leu Thr
305 310 315 320

Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr Ile Pro Gly Thr Thr
325 330 335

Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg Lys Ile Arg Asp Val
340 345 350

Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val Phe His Ala Leu Ser
355 360 365

Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro Asp Asp Glu Gly Lys
370 375 380

Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val Thr Glu His Ser Cys
385 390 395 400

Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val Gln Asn Phe Asp Lys
405 410 415

Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu Thr Glu Glu Lys Gln
420 425 430

Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe His Gln His Cys Ser
435 440 445

Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp Glu Leu Thr His Phe
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Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His Asp Ser Arg Arg Leu
465   470   475   480

Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val Met Ala Asp Phe Ser
                485   490   495

Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe Ile Gln Glu Glu Gln
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Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu Ile Gln Gln Val Glu
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Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile Glu Met Ser Ile Pro
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Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile Ile Ala Pro Met Leu
545   550   555   560

Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys Ala Glu Gln Cys Ala
                565   570   575

Gly His Pro Asn Gly Tyr Cys His Val Ala Phe Gly Ser Ala Lys Ser
            580   585   590

Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala Lys Gly Gly Gly Leu
        595   600   605

Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu Gly Thr Gly Lys Tyr
    610   615   620

Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly Ala Arg Ala His Phe
625   630   635   640

Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys Ile Leu Gln Ser Gly
                645   650   655

Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn Ser Ile Leu Ser Leu
            660   665   670

Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp Leu Ser Val Ile Asp
        675   680   685

Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile Gly Ser Thr Pro Ser
    690   695   700

Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val Gln Ala Ser Asn Leu
705   710   715   720

Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp Val Val Ser Glu Gln
725 730 735

Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser Asp Gly Ile Phe Glu
740 745 750

Gly Pro Arg His Val Glu Asn His Asp Leu Trp Met Lys Arg Lys Leu
755 760 765

Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile Ala Asp Leu Ile Met
770 775 780

Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile Glu Asp Asp Met Thr
785 790 795 800

Val Ile Val Ile Lys Leu Asp His Asn Thr Pro Lys Trp Ala Ser Ile
805 810 815

Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu Ile Ser
820 825

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ttcaaaaccg ctgcccaaaa cgtaacggag ctgccgatca gagaagtctc aaaaggaaaa 180
tatgaaggat attggaccgc tacttcaact gcaaaagcaa aaggagcgga aatcgaggtc 240
atcgtcagag atgattacgg caatgaaacg agacaaacgg caaaaggcaa gctgtatatc 300
aatgaaaagc tgaaataaag gtgaaaagac gctgtcttta atggcagcgt ttttttcgtt 360
ttacgatcga caaattcagt acgaaaactt caaaaaatgt acgatttacg caacattaat 420
tgacagactt tacctttggg cttgatttat acttaggaaa acaaacacta aggtcaccga 480
gccgcagaaa ggggaaggat gtg gaa atc tat tta gat gcg ata tgg ctg tta 533
Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu
1 5 10

aac ttt tgt ttt gac ttg ctg ctt tta atg atg acc gca ttt att tta 581
Asn Phe Cys Phe Asp Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu
15 20 25

aag cga agg gtt aaa aag cgg agg ctg atc cta ggg gca ttt gtc gcg 629
Lys Arg Arg Val Lys Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala
30 35 40

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tca agc atc gtt ctg ttt atg ttt aca cct ttt tca ccg tac gtc ctt      677
Ser Ser Ile Val Leu Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu
    45                  50                  55

cat cct gcc ggc aaa ctg tcg ttt tcg gtt gtg atc gtt ctt gtg gca      725
His Pro Ala Gly Lys Leu Ser Phe Ser Val Val Ile Val Leu Val Ala
60                  65                  70                  75

ttt ggt ttt aag cgg ttc cgg ttt ttt ttg cag aat ttg ttt tct ttt      773
Phe Gly Phe Lys Arg Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe
                80                  85                  90

tat ttt gcc act ttt tta atg gga gga ggg att atc gga gcg cat tct      821
Tyr Phe Ala Thr Phe Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser
            95                  100                 105

ttg ctt gaa acg gat tcg atc atg gaa aac ggc gtc ttt atg acg aat      869
Leu Leu Glu Thr Asp Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn
        110                 115                 120

tgg tcc ggt ttt gga gac ccc gtc agc tgg ctg ttt gtc tgt gtg ggt      917
Trp Ser Gly Phe Gly Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly
    125                 130                 135

ttt gcg gct gta tgg ctg ttt tca aaa aag cgt ttt gaa gat gct gaa      965
Phe Ala Ala Val Trp Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu
140                 145                 150                 155

gcg aag aaa att caa tac gaa gaa cgc gtc cgc cta gag gcc tgc att     1013
Ala Lys Lys Ile Gln Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile
                160                 165                 170

ggt gaa cat acg ctt cat ttc acc gga ttg att gac tcc gga aac cag     1061
Gly Glu His Thr Leu His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln
            175                 180                 185

ctc tac gat cca atc aca aaa acg ccc gtc atg atc gtc aat att gaa     1109
Leu Tyr Asp Pro Ile Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu
        190                 195                 200

aaa ttg aaa gtt gta ttg gga gaa gag gca agt gtg acc atc aag gaa     1157
Lys Leu Lys Val Val Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu
    205                 210                 215

atg agc ccg ctt gat gcc gtc ggg aaa ctg gat gaa gca ctg ccg tat     1205
Met Ser Pro Leu Asp Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr
220                 225                 230                 235

atc ggg cgg atc cgc ctg att ccg tac cgc ggg gtc ggc cat cag cat     1253
Ile Gly Arg Ile Arg Leu Ile Pro Tyr Arg Gly Val Gly His Gln His
                240                 245                 250

cag ttt ctg ctc tgc tta aag ccg gat cat gtg ctc gtt tgt acg gaa     1301
Gln Phe Leu Leu Cys Leu Lys Pro Asp His Val Leu Val Cys Thr Glu
            255                 260                 265

aga gaa gtg att gaa gcg ccg aaa tgc ctg att ggc atc agc aca tca     1349
Arg Glu Val Ile Glu Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser
        270                 275                 280

ccg ctt tcc gct gac ggc gaa ttt gac gcc atc gtc cat ccg aaa atg     1397
Pro Leu Ser Ala Asp Gly Glu Phe Asp Ala Ile Val His Pro Lys Met
    285                 290                 295

ctg gcc gga aac ccg gtc aaa cac gtt tct taaacttgaa gtctgttaca       1447
Leu Ala Gly Asn Pro Val Lys His Val Ser
300                 305
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ttatcatact cctgaagacg tttatttaga agggggagga agatgaaaaa actaaaatta 1507

aggttaacct atctatggta caaactttta atgaaactgg ggctgaaaag cgacgaaatt 1567

tattatatcg gcggaagcga ggcgcttccc ccgccattgt caaaagatga agagcaggtg 1627

cttctccata agctgcctga cggtgatcag gcggcacgag cgattttgat tgaacgaaat 1687

ctcagactgg tcgtgtacat cgcgagaaaa tttgaaaata caggaatcaa tatcgaggat 1747

ttaatctcca tcggcacgat cgggctcatc aaagcggtga atacgtttaa tcccgagaaa 1807

aaaatcaaac tggctacata tgcttccaga tgcattgaaa atgaaatttt gatgtattta 1867

agaagaaaca ataaaatccg ttcagaggta tcattcgacg aaccgctgaa catcgattgg 1927

g 1928

<210> 51
<211> 309
<212> PRT
<213> Bacillus licheniformis

<400> 51

Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu Asn Phe Cys Phe Asp
1 5 10 15

Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu Lys Arg Arg Val Lys
20 25 30

Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala Ser Ser Ile Val Leu
35 40 45

Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu His Pro Ala Gly Lys
50 55 60

Leu Ser Phe Ser Val Val Ile Val Leu Val Ala Phe Gly Phe Lys Arg
65 70 75 80

Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe Tyr Phe Ala Thr Phe
85 90 95

Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser Leu Leu Glu Thr Asp
100 105 110

Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn Trp Ser Gly Phe Gly
115 120 125

Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly Phe Ala Ala Val Trp
130 135 140

Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu Ala Lys Lys Ile Gln
145 150 155 160

Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile Gly Glu His Thr Leu
165 170 175

His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln Leu Tyr Asp Pro Ile
180 185 190

Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu Lys Leu Lys Val Val
195 200 205

Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu Met Ser Pro Leu Asp
210 215 220

Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr Ile Gly Arg Ile Arg
225 230 235 240

Leu Ile Pro Tyr Arg Gly Val Gly His Gln His Gln Phe Leu Leu Cys
245 250 255

Leu Lys Pro Asp His Val Leu Val Cys Thr Glu Arg Glu Val Ile Glu
260 265 270

Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser Pro Leu Ser Ala Asp
275 280 285

Gly Glu Phe Asp Ala Ile Val His Pro Lys Met Leu Ala Gly Asn Pro
290 295 300

Val Lys His Val Ser
305

<210> 52
<211> 1922
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1421)

<400> 52
cggctctttt tttgctgtct gaaatctttt acctctcaca tgccaaatag aaaaatcgga 60

agactacttt ttcaaaggag agcatagagt gtaaaaaaag aggaagtgtt actggaggtt 120

taagatcatg aagcttttct ttggacaagt caatccgacg gttttgacaa tggcggcgtt 180

aagggtggta tcatctttga tcgaactgac ggcggctgtt gtgatgcttt tgacaaacga 240

cgtcagaaaa gctgtggcgg tcaacagcgt actggccatg gtcgggccgc tcatctttat 300

tattacaatg acaatcggca tctatcagat tgcagggcag ctttcttacg caaagctgat 360

tttgatcttt atgggagtgg ttttgatcat cgcggggatc tataaatagc gacacatgat 420

aagagaggcc gacttgtcat aatgtcttcc tttgatcata catttttata gaagacaagc 480

aaaaagagga gggagtgttt ttg cac cac atc aca gag att ctc ccc gat acg 533
Leu His His Ile Thr Glu Ile Leu Pro Asp Thr
1 5 10

atc aaa cgc gcg ctc agc ggt ctt ggc gac cat gaa atc gat cag ata 581
Ile Lys Arg Ala Leu Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile
15 20 25

gaa gaa att cgg gtt cgg aca agt cgt ccg ctg gaa ctg gtg aac aaa 629
Glu Glu Ile Arg Val Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys
30 35 40

gga aag ccg cgc ttt ctc cct tat gtg gcg acg cct gaa gac tcg gcg 677
Gly Lys Pro Arg Phe Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala
45 50 55

ctt ctt tta aac aga ttg gga aat tac agc atg tat aca ctg gaa gag 725
Leu Leu Leu Asn Arg Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu
60 65 70 75

gaa ttg aaa aaa gga tat gtc acg atc aga ggc gga cac cgc gtg ggg 773
Glu Leu Lys Lys Gly Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly
80 85 90

ctt gcc ggc cgg gtt gtc gtc gaa aac ggg gcc gtc aaa gga atc aga 821
Leu Ala Gly Arg Val Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg
95 100 105

gaa ata tca tca ttt aat att cgc att gcc aaa gaa aaa atc ggc att 869
Glu Ile Ser Ser Phe Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile
110 115 120

tcc aaa ccg tat gtc ccc cat tta ttt caa aac tcg tgg ctg aac acg 917
Ser Lys Pro Tyr Val Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr
125 130 135

ctg att atc ggt ccg ccg caa acc gga aaa aca aca ctg ctc aga gac 965
Leu Ile Ile Gly Pro Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp
140 145 150 155

ctc gcc agg ctg atc agt tcg gga agc ggc aac gcc cct gcc aaa aaa 1013
Leu Ala Arg Leu Ile Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys
160 165 170

gtg ggg att gtt gac gaa agg tct gaa atc gca ggc tgt gta aac ggc 1061
Val Gly Ile Val Asp Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly
175 180 185

ata ccg caa tat cgg ctc ggc gac cgg gca gac atc ctt gac gcc tgt 1109
Ile Pro Gln Tyr Arg Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys
190 195 200

cca aaa gcg gaa ggg ctg atg atg atg atc aga tcg atg agt ccg gag 1157
Pro Lys Ala Glu Gly Leu Met Met Met Ile Arg Ser Met Ser Pro Glu
205 210 215

gta atg atc gcc gat gag atc ggg aga atg gaa gac gca gaa gcg ctc 1205
Val Met Ile Ala Asp Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu
220 225 230 235

ttg gaa gcg gtc cac gcg ggg gtg act gtc atc gtt tcg gct cac ggc 1253
Leu Glu Ala Val His Ala Gly Val Thr Val Ile Val Ser Ala His Gly
240 245 250

tac aca tat gca gat ctc gcc agg cgt cca tca ttg aaa atg ctt caa 1301
Tyr Thr Tyr Ala Asp Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln
255 260 265

gag cac cgg gtt ttt gag cga atc gtg gaa ctt tcc aga aag aac ggt 1349
Glu His Arg Val Phe Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly
270 275 280

ccc ggc agc ctg agc cgc atc cta aat ggg aac gga gag ccg ctc ggg 1397
Pro Gly Ser Leu Ser Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly
285 290 295

gca gca aag agg atg tta tca tgc tgaagctttt aggtgccgtg cttattttgg 1451
Ala Ala Lys Arg Met Leu Ser Cys
300 305

cagcagccac atggacagga tttgaaatgg cgaagccttt cagggaaagg ccgaagcaaa 1511

tccgccagct gttggccgct ttgcagtctt tggaggctga aatcatgtac gggcatacac 1571

cgctccgtca ggcatcaaaa cagatcgcac accagcttac cgagccggta gcctctttgt 1631

ttcagacatt tgcagaacag cttgaaaaag gcagcgcttc agcagggacg gcatgggaag 1691

acagcctgga gaaagtatgg cccgaaacgg ctcttaaaaa gaaagaatac gagattttac 1751

ggcaattcgg cgaaacgctg ggccgtcatg atctgatttc tcagcaaaaa catatcaaac 1811

tggcgttaac ccatttagag acagaggaag ctgaagcaaa tctcgcccag gcgaaaaatg 1871

aaaaaatggt caaaagcctt ggatttttga cgggactgct actgattctt c 1922

<210> 53
<211> 307
<212> PRT
<213> Bacillus licheniformis

<400> 53

Leu His His Ile Thr Glu Ile Leu Pro Asp Thr Ile Lys Arg Ala Leu
1 5 10 15

Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile Glu Glu Ile Arg Val
20 25 30

Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys Gly Lys Pro Arg Phe
35 40 45

Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala Leu Leu Leu Asn Arg
50 55 60

Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu Glu Leu Lys Lys Gly
65 70 75 80

Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly Leu Ala Gly Arg Val
85 90 95

Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg Glu Ile Ser Ser Phe
100 105 110

Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile Ser Lys Pro Tyr Val
115 120 125

Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr Leu Ile Ile Gly Pro
130 135 140

Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp Leu Ala Arg Leu Ile
145 150 155 160

Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys Val Gly Ile Val Asp
165 170 175

Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly Ile Pro Gln Tyr Arg
180 185 190

Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys Pro Lys Ala Glu Gly
195 200 205

Leu Met Met Met Ile Arg Ser Met Ser Pro Glu Val Met Ile Ala Asp
210 215 220

Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu Leu Glu Ala Val His
225 230 235 240

Ala Gly Val Thr Val Ile Val Ser Ala His Gly Tyr Thr Tyr Ala Asp
245 250 255

Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln Glu His Arg Val Phe
260 265 270

Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly Pro Gly Ser Leu Ser
275 280 285

Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly Ala Ala Lys Arg Met
290 295 300

Leu Ser Cys
305

<210> 54
<211> 1511
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (498)..(1010)

<220>
<221> CDS
<222> (1036)..(1239)

<220>
<221> CDS
<222> (1255)..(1509)

<400> 54
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agttcgggaa gcggcaacgc ccctgccaaa aaagtgggga ttgttgacga aaggtctgaa 120

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atcgcaggct gtgtaaacgg cataccgcaa tatcggctcg gcgaccgggc agacatcctt     180

gacgcctgtc caaaagcgga agggctgatg atgatgatca gatcgatgag tccggaggta     240

atgatcgccg atgagatcgg gagaatggaa gacgcagaag cgctcttgga agcggtccac     300

gcgggggtga ctgtcatcgt ttcggctcac ggctacacat atgcagatct cgccaggcgt     360

ccatcattga aaatgcttca agagcaccgg gtttttgagc gaatcgtgga actttccaga     420

aagaacggtc ccggcagcct gagccgcatc ctaaatggga acggagagcc gctcggggca     480

gcaaagagga tgttatc atg ctg aag ctt tta ggt gcc gtg ctt att ttg        530
                   Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu
                   1               5                   10

gca gca gcc aca tgg aca gga ttt gaa atg gcg aag cct ttc agg gaa       578
Ala Ala Ala Thr Trp Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu
            15                  20                  25

agg ccg aag caa atc cgc cag ctg ttg gcc gct ttg cag tct ttg gag       626
Arg Pro Lys Gln Ile Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu
        30                  35                  40

gct gaa atc atg tac ggg cat aca ccg ctc cgt cag gca tca aaa cag       674
Ala Glu Ile Met Tyr Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln
    45                  50                  55

atc gca cac cag ctt acc gag ccg gta gcc tct ttg ttt cag aca ttt       722
Ile Ala His Gln Leu Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe
60                  65                  70                  75

gca gaa cag ctt gaa aaa ggc agc gct tca gca ggg acg gca tgg gaa       770
Ala Glu Gln Leu Glu Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu
                80                  85                  90

gac agc ctg gag aaa gta tgg ccc gaa acg gct ctt aaa aag aaa gaa       818
Asp Ser Leu Glu Lys Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu
            95                  100                 105

tac gag att tta cgg caa ttc ggc gaa acg ctg ggc cgt cat gat ctg       866
Tyr Glu Ile Leu Arg Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu
        110                 115                 120

att tct cag caa aaa cat atc aaa ctg gcg tta acc cat tta gag aca       914
Ile Ser Gln Gln Lys His Ile Lys Leu Ala Leu Thr His Leu Glu Thr
    125                 130                 135

gag gaa gct gaa gca aat ctc gcc cag gcg aaa aat gaa aaa atg gtc       962
Glu Glu Ala Glu Ala Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val
140                 145                 150                 155

aaa agc ctt gga ttt ttg acg gga ctg cta ctg att ctt cta ttg atg      1010
Lys Ser Leu Gly Phe Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met
                160                 165                 170

taatgaagag gggagcatac acgaa atg gga gta gac gta aat att att ttt      1062
                            Met Gly Val Asp Val Asn Ile Ile Phe
                                        175                 180

caa att gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg      1110
Gln Ile Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu
                185                 190                 195

gat caa atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga      1158
Asp Gln Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly
            200                 205                 210
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ttc att tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc 1206
Phe Ile Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe
215 220 225

caa aag ata aaa gct gtc ttt cta ttt caa gga taggggggct cactc att 1257
Gln Lys Ile Lys Ala Val Phe Leu Phe Gln Gly Ile
230 235 240

gaa atc gtt caa atc gta gga ctg gga atg atc gcc acc ttc ctc agc 1305
Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu Ser
245 250 255

ttg att gtg aaa gag caa aaa ccg acg ttt gct ttt ttg att gtc gtt 1353
Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val Val
260 265 270

ttt gcc ggc tgc acg att ttt tta ttc tta gta gat cag gtc tac gaa 1401
Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr Glu
275 280 285

atc att cgg atg att gaa aaa ata gct gcc aat gcc aac atc aac atg 1449
Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn Met
290 295 300

atg tat gtc gaa acg att ttg aag att atc ggg att gct tat att gcg 1497
Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile Ala
305 310 315 320

gag ttt ggc gcc ca 1511
Glu Phe Gly Ala

<210> 55
<211> 171
<212> PRT
<213> Bacillus licheniformis

<400> 55

Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu Ala Ala Ala Thr Trp
1 5 10 15

Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu Arg Pro Lys Gln Ile
20 25 30

Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu Ala Glu Ile Met Tyr
35 40 45

Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln Ile Ala His Gln Leu
50 55 60

Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe Ala Glu Gln Leu Glu
65 70 75 80

Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu Asp Ser Leu Glu Lys
85 90 95

Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu Tyr Glu Ile Leu Arg
100 105 110

Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu Ile Ser Gln Gln Lys
115 120 125

His Ile Lys Leu Ala Leu Thr His Leu Glu Thr Glu Glu Ala Glu Ala
130 135 140

Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val Lys Ser Leu Gly Phe
145 150 155 160

Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met
165 170

<210> 56
<211> 68
<212> PRT
<213> Bacillus licheniformis

<400> 56

Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile Ala Gly Val Gly Ile
1 5 10 15

Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
50 55 60

Leu Phe Gln Gly
65

<210> 57
<211> 85
<212> PRT
<213> Bacillus licheniformis

<400> 57

Ile Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu
1 5 10 15

Ser Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val
20 25 30

Val Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr
35 40 45

Glu Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn
50 55 60

Met Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile
65 70 75 80

Ala Glu Phe Gly Ala
85

<210> 58
<211> 1207
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(704)

<400> 58
agccacatgg acaggatttg aaatggcgaa gcctttcagg gaaaggccga agcaaatccg 60

ccagctgttg gccgctttgc agtctttgga ggctgaaatc atgtacgggc atacaccgct 120

ccgtcaggca tcaaaacaga tcgcacacca gcttaccgag ccggtagcct ctttgtttca 180

gacatttgca gaacagcttg aaaaaggcag cgcttcagca gggacggcat gggaagacag 240

cctggagaaa gtatggcccg aaacggctct taaaaagaaa gaatacgaga ttttacggca 300

attcggcgaa acgctgggcc gtcatgatct gatttctcag caaaaacata tcaaactggc 360

gttaacccat ttagagacag aggaagctga agcaaatctc gcccaggcga aaaatgaaaa 420

aatggtcaaa agccttggat ttttgacggg actgctactg attcttctat tgatgtaatg 480

aagaggggag catacacgaa atg gga gta gac gta aat att att ttt caa att 533
Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile
1 5 10

gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg gat caa 581
Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu Asp Gln
15 20 25

atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga ttc att 629
Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile
30 35 40

tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc caa aag 677
Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys
45 50 55

ata aaa gct gtc ttt cta ttt caa gga taggggggct cactcattga 724
Ile Lys Ala Val Phe Leu Phe Gln Gly
60 65

aatcgttcaa atcgtaggac tgggaatgat cgccaccttc ctcagcttga ttgtgaaaga 784

gcaaaaaccg acgtttgctt ttttgattgt cgtttttgcc ggctgcacga ttttttttatt 844

cttagtagat caggtctacg aaatcattcg gatgattgaa aaaatagctg ccaatgccaa 904

catcaacatg atgtatgtcg aaacgatttt gaagattatc gggattgctt atattgcgga 964

gtttggcgcc cagctgacaa aggatgccgg acagggtgcg attgcttcga agatcgaatt 1024

ggcaggcaaa atcctcatct tagtcatggc tgtgcctatt ttaaccgtga ttatcgaaac 1084

gatcatcgga ctcatccctt ccatgtctta gtcagaaagg aggatttcct gagtgaagcg 1144

ttttctgttc tggctcttgg tcatcggaat cgtatgcttt ggagcgcata atgtacaagc 1204

ttc 1207

<210> 59
<211> 68
<212> PRT
<213> Bacillus licheniformis

<400> 59

Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile Ala Gly Val Gly Ile
1 5 10 15

Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
50 55 60

Leu Phe Gln Gly
65

<210> 60
<211> 2153
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1703)

<400> 60
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ttcaaggata ggggggctca ctcattgaaa tcgttcaaat cgtaggactg ggaatgatcg 120

ccaccttcct cagcttgatt gtgaaagagc aaaaaccgac gtttgctttt ttgattgtcg 180

tttttgccgg ctgcacgatt tttttattct tagtagatca ggtctacgaa atcattcgga 240

tgattgaaaa aatagctgcc aatgccaaca tcaacatgat gtatgtcgaa acgattttga 300

agattatcgg gattgcttat attgcggagt ttggcgccca gctgacaaag gatgccggac 360

agggtgcgat tgcttcgaag atcgaattgg caggcaaaat cctcatctta gtcatggctg 420

tgcctatttt aaccgtgatt atcgaaacga tcatcggact catcccttcc atgtcttagt 480

cagaaaggag gatttcctga gtg aag cgt ttt ctg ttc tgg ctc ttg gtc atc 533
Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile
1 5 10

gga atc gta tgc ttt gga gcg cat aat gta caa gct tcg cca aaa gaa 581
Gly Ile Val Cys Phe Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu
15 20 25

gcg gag ccg gct ggg gaa acc gct gca gaa gaa tcg gca gaa gcc att 629
Ala Glu Pro Ala Gly Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile

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        30                      35                      40

gca aga gag cag gct gaa ggt ttg gaa cta gac cgg gtc ggg gag ttc      677
Ala Arg Glu Gln Ala Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe
    45                  50                  55

tgg aac aac att ttg aca gag tat ggg gga cac ctt ccc gaa agt caa      725
Trp Asn Asn Ile Leu Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln
60                  65                  70                  75

aaa gga agc ctg ctt gaa ttt gtc aaa gga gaa aag cac ttt tcg cct      773
Lys Gly Ser Leu Leu Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro
                80                  85                  90

gag gaa tgg ggc aaa gcg ctg ttt tcc tac ttg ttc cat gaa gtg ctg      821
Glu Glu Trp Gly Lys Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu
            95                  100                 105

gct aac ggg aaa ctg ctg ggg acg ctg atc ctg ttg acc atc ttc tgc      869
Ala Asn Gly Lys Leu Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys
        110                 115                 120

gtc ctg ctt cag ctt ttg caa aac gcg ttt caa caa agc acc gtc agc      917
Val Leu Leu Gln Leu Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser
    125                 130                 135

aaa gtg gcg tat gca att gtc tac atg gtg ctg att att ctt gcg ctc      965
Lys Val Ala Tyr Ala Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu
140                 145                 150                 155

aac agc ttt cgg gtt gcc gtc aca tat gcg aat gaa gcg att cag acg     1013
Asn Ser Phe Arg Val Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr
                160                 165                 170

atg aca agc ttt atc ctg tcg ctc gta cct ctg ctt ctg gcg ctg atg     1061
Met Thr Ser Phe Ile Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met
            175                 180                 185

gcg act tcg ggg gga gcc gcc tca gcc gca ttc ttt cat ccg gtc att     1109
Ala Thr Ser Gly Gly Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile
        190                 195                 200

ctt ttt ctc atg aac acg agc ggc ttg ttt atc caa tat atc gtg ttg     1157
Leu Phe Leu Met Asn Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu
    205                 210                 215

ccg ctt tta ttt tta tca gcg att tta agc att gtc agc acg atg acg     1205
Pro Leu Leu Phe Leu Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr
220                 225                 230                 235

gac caa tat aaa gtc aca cag ctg gcc cag ctc ctc aga aat gcg gcg     1253
Asp Gln Tyr Lys Val Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala
                240                 245                 250

atc ggc acg ctg gct gca ttt ttg acc gta ttc ctc ggt gtc atc tcg     1301
Ile Gly Thr Leu Ala Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser
            255                 260                 265

gtt cag ggc gcc tca gcc gca gtg acg gac ggc att act ttg cgg acg     1349
Val Gln Gly Ala Ser Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr
        270                 275                 280

gca aaa ttc att acc gga aac ttc atc ccc gta ttg ggc cgc atg ttt     1397
Ala Lys Phe Ile Thr Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe
    285                 290                 295

acc gaa gcg aca gac acg gtg atc agc gcg tct ctc ctg ctg aaa aac     1445
Thr Glu Ala Thr Asp Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn
```

300 305 310 315

acc gtc ggg ata ctc ggt gtg gca atc tta att tgc atc gca gcc ttt 1493
Thr Val Gly Ile Leu Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe
320 325 330

ccc gcg atc aaa atc ctt tcc ctc gcg ctc ata tac aaa att gcc gcg 1541
Pro Ala Ile Lys Ile Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala
335 340 345

gcg gtt ctc cag cct ctc gga ggc ggc ccg gtt atc agc tgc ctg gat 1589
Ala Val Leu Gln Pro Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp
350 355 360

gtc atc agc aaa agc gtc atc tac att ttc gcg gcc atg gcc atc gtt 1637
Val Ile Ser Lys Ser Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val
365 370 375

tcg ctg atg ttt ttc tta agc tta acc gtg atc att aca gcg ggg aat 1685
Ser Leu Met Phe Phe Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn
380 385 390 395

ctg acg atg atg atg aag tagggaggga tgagatggaa tttctgacag 1733
Leu Thr Met Met Met Lys
400

agtggctcac gaatattatt ctatttattc tgatggcgat cgtcatcgat atgcttctgc 1793

cgaattcgag catgcaaaaa tacgcgaaaa tggtgatcag cctgctcttg atcgttgtaa 1853

tactgaaccc gatcttctct ttattcagga cagatccgga tgtgattttt gagaagctta 1913

caaaaaacgg acaagttcag tcaaacgaaa taaaaaatca gctgaattca gaaaaaaaag 1973

aaatacaagc ctcacaacaa gcatatatct tagaacagat ggctgttcaa ttggaaaaga 2033

acgcagaggg caggtttaca agcgacaaat acaagataga ccgagtcgag gtctcttctg 2093

acagccagct gaaaacagag aaagacctca gtaagcatgc ggaagtctcg gtattcttga 2153

<210> 61
<211> 401
<212> PRT
<213> Bacillus licheniformis

<400> 61

Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile Gly Ile Val Cys Phe
1 5 10 15

Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu Ala Glu Pro Ala Gly
20 25 30

Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile Ala Arg Glu Gln Ala
35 40 45

Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe Trp Asn Asn Ile Leu
50 55 60

Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln Lys Gly Ser Leu Leu
65 70 75 80

Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro Glu Glu Trp Gly Lys
85 90 95

Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu Ala Asn Gly Lys Leu
100 105 110

Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys Val Leu Leu Gln Leu
115 120 125

Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser Lys Val Ala Tyr Ala
130 135 140

Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu Asn Ser Phe Arg Val
145 150 155 160

Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr Met Thr Ser Phe Ile
165 170 175

Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met Ala Thr Ser Gly Gly
180 185 190

Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile Leu Phe Leu Met Asn
195 200 205

Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu Pro Leu Leu Phe Leu
210 215 220

Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr Asp Gln Tyr Lys Val
225 230 235 240

Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala Ile Gly Thr Leu Ala
245 250 255

Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser Val Gln Gly Ala Ser
260 265 270

Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr Ala Lys Phe Ile Thr
275 280 285

Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe Thr Glu Ala Thr Asp
290 295 300

Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn Thr Val Gly Ile Leu
305 310 315 320

Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe Pro Ala Ile Lys Ile
325 330 335

Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala Ala Val Leu Gln Pro
340 345 350

Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp Val Ile Ser Lys Ser
355 360 365

Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val Ser Leu Met Phe Phe
370 375 380

Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn Leu Thr Met Met Met
385 390 395 400

Lys

<210> 62
<211> 1696
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1193)

<400> 62
cttgatcgtt gtaatactga acccgatctt ctctttattc aggacagatc cggatgtgat 60

ttttgagaag cttacaaaaa acggacaagt tcagtcaaac gaaataaaaa atcagctgaa 120

ttcagaaaaa aaagaaatac aagcctcaca acaagcatat atcttagaac agatggctgt 180

tcaattggaa aagaacgcag agggcaggtt tacaagcgac aaatacaaga tagaccgagt 240

cgaggtctct tctgacagcc agctgaaaac agagaaagac ctcagtaagc atgcggaagt 300

ctcggtattc ttgaaaccag catcggaaaa aacggtccaa gccgtcgctc ctgtcgagat 360

caatacggac cggagctacc agtccatgca ggaaagagaa aagaaagaga cgggggaagt 420

cagagaacag ctagcaggca tctgggaaat aagccccgac aagattacag ttcatatcga 480

aggggggagaa cgaagcggca atg aat aaa aga acc tgg atc gaa aag ctg atc 533
Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile
1 5 10

ggc cac ctg ctc ccg aaa gac gag aaa gac gga aaa aag ctg acg aaa 581
Gly His Leu Leu Pro Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys
15 20 25

tat cac tac ttt ctg ctg ctt ttt gtt ctc ggc gtt tcc ttc atg ctc 629
Tyr His Tyr Phe Leu Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu
30 35 40

gtc agc cag atc ttc tct tcc gaa cct tcc caa gag cca gcg gca gat 677
Val Ser Gln Ile Phe Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp
45 50 55

cag ccg gcg gct tca caa aaa gct acg tct gaa agc acc gta cag agc 725
Gln Pro Ala Ala Ser Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser
60 65 70 75

ggt gaa gga gaa aaa gaa gtg ttc aag ccc gcc tca gat gac aaa ccg 773
Gly Glu Gly Glu Lys Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro
80 85 90

aag gaa tcg atc caa gat tac gaa cag gaa tat gaa aat cag ctc aaa 821

Lys Glu Ser Ile Gln Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys
95 100 105

gac ata ttg gaa acc atc atc ggc gtt gag gac gtg tca atc gtc gtc 869
Asp Ile Leu Glu Thr Ile Ile Gly Val Glu Asp Val Ser Ile Val Val
110 115 120

aat gtt gat gca acc tca ttg aaa ata ttc gag aaa aac aga aaa acc 917
Asn Val Asp Ala Thr Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr
125 130 135

cag gaa act tca acg aat gag aca gat aaa cag gga ggc aag cgg acg 965
Gln Glu Thr Ser Thr Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr
140 145 150 155

gtg tct gaa atg tct tca gac gaa gaa atc gtc atc atc aaa aac gga 1013
Val Ser Glu Met Ser Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly
160 165 170

gat aaa gag acg cct gtc gtc gtt cag acg aaa aag ccc gat atc agg 1061
Asp Lys Glu Thr Pro Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg
175 180 185

ggt gtt ctc gtt gtc gct cag gga gtc gac aac gtt caa ata aaa aag 1109
Gly Val Leu Val Val Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys
190 195 200

acc att att gaa gca gtg aca agg gtt ctt gat gtt ccg agc cac cgc 1157
Thr Ile Ile Glu Ala Val Thr Arg Val Leu Asp Val Pro Ser His Arg
205 210 215

gtc gct gtt gcc cct aaa aaa atg aag gag gat tca taaatgatgc 1203
Val Ala Val Ala Pro Lys Lys Met Lys Glu Asp Ser
220 225 230

tgaaaaaaca aacggtttgg cttttaacca tgttaagtct cgtcgttgta ctgagtgtct 1263

actacattat gtcgcccgaa ggagaaaatg tcgtcacggt tgatgacaag gaacaagttg 1323

ccgctgaaaa agaaaaaccg atgaaagaag agcctgccaa ggatggcaaa gatgataccg 1383

cgcctgctaa agacaaaact aaagggaaag atacaaaaga taaagaaacg tctgcgagtg 1443

agcagaacgg agaggttgtc acagaggaat catcgggtga tgaagattta ttcacaacat 1503

accgcatgga aatggacgat cagcgcagca gggagaggga ggaattaacc gaaatcgtca 1563

gaagcgataa agcgacggca aaagaaaaaa gcgaagctta cgacaagatg acagagctca 1623

gcgaagctga aggaacggaa aagacccttg aaaccctcat caaaacaaaa ggctattaag 1683

acgccttggt caa 1696

<210> 63
<211> 231
<212> PRT
<213> Bacillus licheniformis

<400> 63

Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile Gly His Leu Leu Pro
1 5 10 15

Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys Tyr His Tyr Phe Leu
20 25 30

Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu Val Ser Gln Ile Phe
35 40 45

Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp Gln Pro Ala Ala Ser
50 55 60

Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser Gly Glu Gly Glu Lys
65 70 75 80

Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro Lys Glu Ser Ile Gln
85 90 95

Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys Asp Ile Leu Glu Thr
100 105 110

Ile Ile Gly Val Glu Asp Val Ser Ile Val Val Asn Val Asp Ala Thr
115 120 125

Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr Gln Glu Thr Ser Thr
130 135 140

Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr Val Ser Glu Met Ser
145 150 155 160

Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly Asp Lys Glu Thr Pro
165 170 175

Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg Gly Val Leu Val Val
180 185 190

Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys Thr Ile Ile Glu Ala
195 200 205

Val Thr Arg Val Leu Asp Val Pro Ser His Arg Val Ala Val Ala Pro
210 215 220

Lys Lys Met Lys Glu Asp Ser
225 230

<210> 64
<211> 1062
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (498)..(980)

<400> 64
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cagatgacaa accgaaggaa tcgatccaag attacgaaca ggaatatgaa aatcagctca 120

aagacatatt ggaaaccatc atcggcgttg aggacgtgtc aatcgtcgtc aatgttgatg 180

caacctcatt gaaaatattc gagaaaaaca gaaaaaccca ggaaacttca acgaatgaga 240

cagataaaca gggaggcaag cggacggtgt ctgaaatgtc ttcagacgaa gaaatcgtca 300

tcatcaaaaa cggagataaa gagacgcctg tcgtcgttca gacgaaaaag cccgatatca 360

ggggtgttct cgttgtcgct cagggagtcg acaacgttca aataaaaaag accattattg 420

aagcagtgac aagggttctt gatgttccga gccaccgcgt cgctgttgcc cctaaaaaaa 480

tgaaggagga ttcataa atg atg ctg aaa aaa caa acg gtt tgg ctt tta 530
Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu
1 5 10

acc atg tta agt ctc gtc gtt gta ctg agt gtc tac tac att atg tcg 578
Thr Met Leu Ser Leu Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser
15 20 25

ccc gaa gga gaa aat gtc gtc acg gtt gat gac aag gaa caa gtt gcc 626
Pro Glu Gly Glu Asn Val Val Thr Val Asp Asp Lys Glu Gln Val Ala
30 35 40

gct gaa aaa gaa aaa ccg atg aaa gaa gag cct gcc aag gat ggc aaa 674
Ala Glu Lys Glu Lys Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys
45 50 55

gat gat acc gcg cct gct aaa gac aaa act aaa ggg aaa gat aca aaa 722
Asp Asp Thr Ala Pro Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys
60 65 70 75

gat aaa gaa acg tct gcg agt gag cag aac gga gag gtt gtc aca gag 770
Asp Lys Glu Thr Ser Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu
80 85 90

gaa tca tcg ggt gat gaa gat tta ttc aca aca tac cgc atg gaa atg 818
Glu Ser Ser Gly Asp Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met
95 100 105

gac gat cag cgc agc agg gag agg gag gaa tta acc gaa atc gtc aga 866
Asp Asp Gln Arg Ser Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg
110 115 120

agc gat aaa gcg acg gca aaa gaa aaa agc gaa gct tac gac aag atg 914
Ser Asp Lys Ala Thr Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met
125 130 135

aca gag ctc agc gaa gct gaa gga acg gaa aag acc ctt gaa acc ctc 962
Thr Glu Leu Ser Glu Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu
140 145 150 155

atc aaa aca aaa ggc tat taagacgcct tggtcaacgc cgacggcgat 1010
Ile Lys Thr Lys Gly Tyr
160

aaagtcaata ttacggtgaa ggcgaaggag cactcgaaag ccgcctgcac cg 1062

<210> 65
<211> 161
<212> PRT
<213> Bacillus licheniformis

<400> 65

Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu Thr Met Leu Ser Leu
1 5 10 15

Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser Pro Glu Gly Glu Asn
20 25 30

Val Val Thr Val Asp Asp Lys Glu Gln Val Ala Ala Glu Lys Glu Lys
35 40 45

Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys Asp Asp Thr Ala Pro
50 55 60

Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys Asp Lys Glu Thr Ser
65 70 75 80

Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu Glu Ser Ser Gly Asp
85 90 95

Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met Asp Asp Gln Arg Ser
100 105 110

Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg Ser Asp Lys Ala Thr
115 120 125

Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met Thr Glu Leu Ser Glu
130 135 140

Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu Ile Lys Thr Lys Gly
145 150 155 160

Tyr

<210> 66
<211> 3346
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(2843)

<400> 66
gtattcaaaa aacaatttaa cccgtgacat cgagacgaat gtcataggaa aaaatgcggt 60

taaatacgga ttaatcgatg aaaaccggcg agagacagac aggcgattca aaagctgatg 120

aatataatcg aacaaaacaa ggacgcacag gaagagataa tccaatgatt ctgtataaaa 180

aaatgccgca ggaaatcgtg ttcgcagggc aggcggaaaa ctcgaactta aaacagatcg 240

atgtaaacag cgtaccactt ttagtcgaga tgaacggaga ggaagcaagg aacgttcaga 300

gttctcagca cgaacccgat ggattttta aaacaagaaa cggcccctgg gcagacgctt 360

aaactgacat tttataaata gctggagtgt ctcaaggata aatatgctat aataggggaa 420

tccagaggaa aatcgcagcc gaaaaaaggc tgctttctct ttgtttttac attttttaac 480

acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa 533
Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys
1 5 10

caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga 581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly
15 20 25

tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta 629
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val
30 35 40

gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg 677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp
45 50 55

ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt 725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe
60 65 70 75

tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt 773
Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu
80 85 90

tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt 821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe
95 100 105

cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa 869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln
110 115 120

aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg 917
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser
125 130 135

cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca 965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser
140 145 150 155

tat ttt ctg ttt gca tct gca gga tct aaa atc atc gcc gtc ttc ctg 1013
Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu
160 165 170

atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg 1061
Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr
175 180 185

ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg 1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp
190 195 200

cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa 1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys
205 210 215

aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct 1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser
220 225 230 235

gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa 1253
Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln
240 245 250

tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa 1301
Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu
255 260 265

gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag 1349
Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu
270 275 280

ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg 1397
Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr
285 290 295

ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg 1445
Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu
300 305 310 315

ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att 1493
Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile
320 325 330

tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt 1541
Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val
335 340 345

aag gcg aaa gtc acc cag gtt cat ctc ggc ccg gcc gtc acg aaa tat 1589
Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr
350 355 360

gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta 1637
Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu
365 370 375

agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa 1685
Ser Asp Asp Leu Ala Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu
380 385 390 395

gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg 1733
Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala
400 405 410

gaa gtg gcg atg gtt tcc ttg aaa gaa gtg ctt gaa tcg aaa ctg aat 1781
Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn
415 420 425

gac cgg ccg gat gca aag ctg atg atc ggc ctc ggc cgg aac att tcc 1829
Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser
430 435 440

gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt 1877
Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val
445 450 455

gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att 1925
Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile
460 465 470 475

aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg 1973
Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met
480 485 490

att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat 2021
Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His
495 500 505

ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg 2069
Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu
510 515 520

aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac 2117
Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His
525 530 535

acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg 2165
Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met
540 545 550 555

aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg 2213
Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val
560 565 570

att gtg gac gag ctt gcc gac ctg atg atg gtc gct tcc tct gat gtt 2261
Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val
575 580 585

gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc 2309
Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile
590 595 600

cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg 2357
His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly
605 610 615

gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct 2405
Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser
620 625 630 635

cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt 2453
Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu
640 645 650

ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg 2501
Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro
655 660 665

ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt 2549
Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val
670 675 680

gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg 2597
Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met
685 690 695

att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt 2645
Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu
700 705 710 715

tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta 2693
Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val
720 725 730

tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg 2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg
735 740 745

ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga 2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly
750 755 760

tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc 2837
Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu
765 770 775

tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac 2893
Ser Ser
780

atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat 2953

ctgatctgtc agacggaggg aaaacatgtc gataaaagct gacaatcaac ggttatgttt 3013

aaaggtgatt gatcggataa aagatgatat tcaaaatggg gtcttttgcg aaaatgaacg 3073

gctcccgagt gaatttgagc tgtcaaagat gcttggtgtg agcagaacgg ctttgcgtga 3133

ggcgcttaga atactggaag aagaaaacgt catcatcaga aggcatggag tcggacattt 3193

tgtaaatgcc agaccgttat ttctatcagg tattgagcag ctgaacagcg tcacaaaaat 3253

gatcgagcag gcaagcatga cgccgggaac catttttatg tcctcacagg ttaccgctcc 3313

cactgaagaa gatatgctcc ggtttcaata tgc 3346

<210> 67
<211> 781
<212> PRT
<213> Bacillus licheniformis

<400> 67

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys
1 5 10 15

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala
20 25 30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe
35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
50 55 60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
145 150 155 160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
165 170 175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
180 185 190

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
325 330 335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
420 425 430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
435 440 445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
450 455 460

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
530 535 540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
580 585 590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
595 600 605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780

<210> 68
<211> 1045
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1043)

<400> 68
tcaaagcggc gggattataa agatatcggc aagctttcga tcgggccggg aatatttaat 60

atcaatgaac ctgtcatttt cggacttccg gtcgtgctca atccaatctt catgattccc 120

tttattatcg ttccggcagt caatactgtc atcggctatt tgttcatcaa gtttcagctg 180

attccgccga tcgcatacgc tgttccgtgg acaacgccag ggccgttgat tccgtttctc 240

gggaccggag gaaactggct tgcgctcggc gtcggctttc tctgcctcgc catttcaacg 300

atgatttatc tgccgtttgt gatggctgcc aacaagactg tgaatacgga cagggagcat 360

tccgcggaaa acaggaagga atcataactt tagacggggc gccttttacg ggcgcccgtc 420

ttttttttaaa aaaagtcatg cggctctctt ttctctcata caatctatta aaatcaaaag 480

cacgtctggg aggaagatac atg cgg aag ccc aca atc aaa gag ctc atc ttt 533
Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe
1 5 10

caa cat atg aag gac cat ctg tcg atc tat tta ttt gtt tct gtg ctg 581
Gln His Met Lys Asp His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu
15 20 25

ttc tta atg ggt gtg att ttc ggc gcg gtc atc gtc aac agc atg acg 629
Phe Leu Met Gly Val Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr
30 35 40

atc ggt caa aaa gaa gat ttg ttc tac tat ttg aat caa ttt ttt gga 677
Ile Gly Gln Lys Glu Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly
45 50 55

cag ctt tcc gaa gga aaa gca gcc agc tca aag gaa atg ttt ttg cag 725
Gln Leu Ser Glu Gly Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln
60 65 70 75

agc ttt ctt cat aat atg aaa tat tta ggc tta atg tgg att ctc ggg 773
Ser Phe Leu His Asn Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly
80 85 90

ata tcc atc atc ggt ctg ccc gtc att ttt atc atg gtc ttc tta aaa 821
Ile Ser Ile Ile Gly Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys
95 100 105

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ggg atc gtc gtc gga ttt aca gtc ggc ttt ttg gtc aat caa atg gga        869
Gly Ile Val Val Gly Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly
        110                 115                     120

atc aac ggc ttt ttc ctg tct ttt gtc tcc gtg ctc ccg caa aat att        917
Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile
    125                 130                 135

ctg ctg atc ccg gcg tac ttg atc atg ggc acc tgc gcc atc gcc ttt        965
Leu Leu Ile Pro Ala Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe
140                 145                 150                     155

tcg atg agg ctc atc cgc cag ctt ttt gta aac gca gcc ttc aga agc       1013
Ser Met Arg Leu Ile Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser
                160                     165                 170

acc tgt cca tgt gtt gtg ccg cgg gta gcc ga                            1045
Thr Cys Pro Cys Val Val Pro Arg Val Ala
            175                 180
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<210> 69
<211> 181
<212> PRT
<213> Bacillus licheniformis

<400> 69

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Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe Gln His Met Lys Asp
1               5                   10                  15

His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu Phe Leu Met Gly Val
            20                  25                  30

Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr Ile Gly Gln Lys Glu
        35                  40                  45

Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly Gln Leu Ser Glu Gly
    50                  55                  60

Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln Ser Phe Leu His Asn
65                  70                  75                  80

Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly Ile Ser Ile Ile Gly
                85                  90                  95

Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys Gly Ile Val Val Gly
            100                 105                 110

Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly Ile Asn Gly Phe Phe
        115                 120                 125

Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile Leu Leu Ile Pro Ala
    130                 135                 140

Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe Ser Met Arg Leu Ile
145                 150                 155                 160
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Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser Thr Cys Pro Cys Val
165 170 175

Val Pro Arg Val Ala
180

<210> 70
<211> 1108
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (500)..(1108)

<400> 70
agtggtcgat gccgtcacga tcacgagcga cacgattgat tacatgctga agcattttgg 60

aagagagatg agagacgaca gtccgtccag gtcgctcgtt cccgcgggga tgagctttgg 120

gaaaagaaag gtcctcaccg aagaagacct tcccgatgaa gagcaccgca aatcgtttct 180

cggtatagtc ggaggcctcg cagaggatga aaaaaggcag ctgatccatg aagtcctcgc 240

tccgctcggc cataacttaa tggtgacccc taaagaggtc gatacattta tcgatgatat 300

ggcaaatgtg attgcaaacg gtctgaacac agcgctccat gaaaatgtat cgcaagacaa 360

taaaggaatg tataaccact aagatcaagg cggctggccc ggccgctttt tttcatgaca 420

tttagcattg ccggaacttg ttctacttcc tctatcttgt acatagtcta tttactagac 480

aagctctgga gggatttac aat gag aaa aag agg cag gaa tcg tca gtt tgt 532
Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys
1 5 10

gct ggc tgt aaa tgg aag aag cgc ggt tca gac agt att ctt att tat 580
Ala Gly Cys Lys Trp Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr
15 20 25

cgt cag cct gct gct cgt ttt tat ttt atc agg cgt gct cac atc gct 628
Arg Gln Pro Ala Ala Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala
30 35 40

gcg tcc tca gtt aag gcc gtc ttc atc gtt gta ccg ggt ggc tca tca 676
Ala Ser Ser Val Lys Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser
45 50 55

act gaa ggg cga gac ctt tgg gct cat ttt ggg aat gga aaa cca cta 724
Thr Glu Gly Arg Asp Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu
60 65 70 75

ctt tgc atc aga att gcc gga acc gaa tca gcg ctt tca gct ttc ccc 772
Leu Cys Ile Arg Ile Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro
80 85 90

cct cgt cct gaa gct ggc gac cag cat tca ttt gaa aga tcc gcg aag 820
Pro Arg Pro Glu Ala Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys
95 100 105

ttt tct cgg acg gga gct tcc ggg att ctc tca ttt tca ctc gga aat 868
Phe Ser Arg Thr Gly Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn
110 115 120

cct cat tgc cgg gca agg gac gga tta tac gaa tat gcc gtc aga atc 916

Pro His Cys Arg Ala Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile
125 130 135

tcc gcc gcc gac tca ggt ctt aaa aga gga gag aga agc gaa tct tgc 964
Ser Ala Ala Asp Ser Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys
140 145 150 155

aga gct tca agg gaa aca gaa aaa gaa aac aga cgg gga aaa acc tcc 1012
Arg Ala Ser Arg Glu Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser
160 165 170

tca aca atc gac ggg cgg ccg caa agt cgt att tat cta caa tac gca 1060
Ser Thr Ile Asp Gly Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala
175 180 185

caa tac gga atc gta tct tcc cct ttt aaa agg tca ggc aga tcc ttt 1108
Gln Tyr Gly Ile Val Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
190 195 200

<210> 71
<211> 203
<212> PRT
<213> Bacillus licheniformis

<400> 71

Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys Ala Gly Cys Lys Trp
1 5 10 15

Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr Arg Gln Pro Ala Ala
20 25 30

Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala Ala Ser Ser Val Lys
35 40 45

Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser Thr Glu Gly Arg Asp
50 55 60

Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu Leu Cys Ile Arg Ile
65 70 75 80

Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro Pro Arg Pro Glu Ala
85 90 95

Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys Phe Ser Arg Thr Gly
100 105 110

Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn Pro His Cys Arg Ala
115 120 125

Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile Ser Ala Ala Asp Ser
130 135 140

Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys Arg Ala Ser Arg Glu
145 150 155 160

Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser Ser Thr Ile Asp Gly

165 170 175

Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala Gln Tyr Gly Ile Val
180 185 190

Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
195 200

<210> 72
<211> 1152
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (107)..(985)

<400> 72
ttgtttttaa ttaaaaacga aacaagctgg tgcaaaatta attgaaaaaa agtttttttgg 60

taaaagtata aatttcatga agagggttca gaatggtgct gaggtg atg agt aag 115
Met Ser Lys
1

aaa gag aaa gag aag aat cgt act tcc aaa atc aca aag ttg caa caa 163
Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys Leu Gln Gln
5 10 15

ttt ttt cgt aaa cgc tgg gta ttt ccg gcc atc tat ttg aca agt gcc 211
Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu Thr Ser Ala
20 25 30 35

gtc gtt gta tta acc gcc gtt cta tgg tat caa tcg gct tct aac aac 259
Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala Ser Asn Asn
40 45 50

gat gta aaa gac cag ctt gca gac gat ggc aag aaa tca gcc tat gat 307
Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser Ala Tyr Asp
55 60 65

aac cgg gat gat gcg gta gaa gta ggc aaa cca gtc gaa aat gtc gca 355
Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu Asn Val Ala
70 75 80

atg ccg gtt gct gat tct gaa aat gtt tcc gtc gtt aaa aag ttt ttt 403
Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys Lys Phe Phe
85 90 95

gaa act gac gca act aaa gaa gag aaa gaa gca gca ctt gta aac tat 451
Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu Val Asn Tyr
100 105 110 115

aat aac acg tac agc atg agc aaa ggt atc gac ttg gct gag aaa gac 499
Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala Glu Lys Asp
120 125 130

gga aaa aca ttt gat gtt tcc gca tct cta agc ggt acg gtc atc aaa 547
Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr Val Ile Lys
135 140 145

gct gca aaa gac cct gta ctg ggc tac gtt gtt gaa gtt gaa cat gaa 595
Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val Glu His Glu
150 155 160

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gat ggt tta tca act gtg tat cag tct ctt tct gaa gta agc gtc aaa        643
Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val Ser Val Lys
    165                 170                 175

caa ggt gac aag att gaa caa aat caa gtc atc gga aaa gca ggc aaa        691
Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys Ala Gly Lys
180                 185                 190                 195

aac ctt tac aat gaa gaa ggc gga aac cat gtg cat ttt gaa atc cgc        739
Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe Glu Ile Arg
                200                 205                 210

aaa gac ggt gtt gcg cta aac ccg ctg aac ttc atg gac aag ccg gtc        787
Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp Lys Pro Val
            215                 220                 225

tcc agc att gaa aaa gca atg gag gaa caa gcg tct gaa gtg aaa gaa        835
Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu Val Lys Glu
        230                 235                 240

cct gct cag cct tct gtt gaa gaa aag tca aaa aca gaa gac aaa gcg        883
Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu Asp Lys Ala
    245                 250                 255

aaa gat caa aca gat gga aaa gac gac aaa acc aag cgg gaa gat tcg        931
Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg Glu Asp Ser
260                 265                 270                 275

tct gaa ggg tca gaa aat caa gac gga acc cag tct gac gat tca agc        979
Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp Asp Ser Ser
                280                 285                 290

cag tca taaggcacgc ttccctcagg gcgcctatca aatgcgatag gcgccttttt        1035
Gln Ser

tgttacaatc aaaaaaaacc cgtatcaaat cggcggagcc agccgttttt aagtaagagg     1095

cctctttaag gagtggaagg cattaggaag taagtagaac agcaaaccgc ctagtaa        1152


<210>  73
<211>  293
<212>  PRT
<213>  Bacillus licheniformis

<400>  73

Met Ser Lys Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys
1               5                   10                  15

Leu Gln Gln Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu
            20                  25                  30

Thr Ser Ala Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala
        35                  40                  45

Ser Asn Asn Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser
    50                  55                  60

Ala Tyr Asp Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu
65                  70                  75                  80
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Asn Val Ala Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys
85 90 95

Lys Phe Phe Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu
100 105 110

Val Asn Tyr Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala
115 120 125

Glu Lys Asp Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr
130 135 140

Val Ile Lys Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val
145 150 155 160

Glu His Glu Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val
165 170 175

Ser Val Lys Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys
180 185 190

Ala Gly Lys Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe
195 200 205

Glu Ile Arg Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp
210 215 220

Lys Pro Val Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu
225 230 235 240

Val Lys Glu Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu
245 250 255

Asp Lys Ala Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg
260 265 270

Glu Asp Ser Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp
275 280 285

Asp Ser Ser Gln Ser
290

<210> 74
<211> 1747
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1244)

<400> 74
gctttaatcg cgggtaactt gcacagtaca accgacatcc cgttctgggt gcagtttgca 60

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tgcgccatgg ccatgggact cggaacatct gtcggcggct ggaaaatcat caaaaccgtc     120

ggcggaaaaa tcatgaagat ccgtcccgtc aacggtgtct ctgcagattt gacgggagcc     180

ctcatcatct ttggcgcgac gatcgtccat ttgcctgtca gcacgacaca cgtcatttct     240

tcatccattt taggcgtggg cgcttcccac cgggtgaaag gcgtaaactg gggcaccgca     300

aagcggatgc tgatcacttg ggtcattacc cttcccattt cggcaaccat cggtgcattt     360

gcctatttca tacttgattt attcttttaa tcagcacact cccgtccgaa tctaggacgg     420

gagttttcat gtttaaaaga aagccggcat aacaatagaa ataggaactg cactatttct     480

cgggaagagg gaaacaagtt atg ctg cta ttt tat caa ttc ctt gtt tgg ctt     533
                      Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu
                      1               5                   10

att gtt ttg gcg ctg gct ctg tac gta gct gcc gtg tgg cgt ttt gaa       581
Ile Val Leu Ala Leu Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu
            15                  20                  25

aaa cag ctc gcc gaa aaa acg gtc gcc atc aga aaa acg tgg tac ctt       629
Lys Gln Leu Ala Glu Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu
        30                  35                  40

ctt tat gtc atc ggc gcc gtg ata tat tgg acg cac gat ccg cag tca       677
Leu Tyr Val Ile Gly Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser
    45                  50                  55

att ttc aca aac ccg ctt cat tac ctg atc gtt gcc gtt ttt ttc acg       725
Ile Phe Thr Asn Pro Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr
60                  65                  70                  75

ttg aca gac gct ttt att ttc tta aat gcc tac ttt aaa aag ctc ggc       773
Leu Thr Asp Ala Phe Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly
                80                  85                  90

agc tct gaa ctc gcg aca gat aca aga atg ctt ctc gaa gaa aac aac       821
Ser Ser Glu Leu Ala Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn
            95                  100                 105

gac ctc ctc cac acg tat caa aac agg ctg aaa acg ttt caa tac cta       869
Asp Leu Leu His Thr Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu
        110                 115                 120

ttg aaa aac gaa ccg atc cac atc tat tat gga aat ata gaa gcg tat       917
Leu Lys Asn Glu Pro Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr
    125                 130                 135

gca gaa ggc atc gaa aag ctc atc aaa cgg ttt gcc gaa aaa atg aat       965
Ala Glu Gly Ile Glu Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn
140                 145                 150                 155

ata tcc gct gca ctt tgc gaa tat aat tca gaa gaa agc aag gat cat      1013
Ile Ser Ala Ala Leu Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His
                160                 165                 170

ttg ctt gag cat atg gaa aac cgg ttc gat gtt caa gaa aag ctt gac      1061
Leu Leu Glu His Met Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp
            175                 180                 185

cgc aaa gac gtt tat tat gaa gaa aac gga aaa atg gtc ctc att cct      1109
Arg Lys Asp Val Tyr Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro
        190                 195                 200

ttt tcc atc cac gat ttt gac tat gtc atg aag tta acc tca gaa gac      1157
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Phe Ser Ile His Asp Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp
205 210 215

ctt gtc aca gaa ttt gat tat ctc ctg ttt act tct tta aca agc atc 1205
Leu Val Thr Glu Phe Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile
220 225 230 235

tat gat ctt ctg cta cca aac gaa gag gaa ggt gac gac tgatggagcc 1254
Tyr Asp Leu Leu Leu Pro Asn Glu Glu Glu Gly Asp Asp
240 245

tgcttttcag caagaccagg aaagcgtaaa aaagcgcctc gcctttaaaa tgtttaaaag 1314

gcaatccaaa accaatatcg cgaaatacga agtcagcccc tataccgaac ggattttccg 1374

gcaaaacgaa cggctgatcg gcgagtataa aagaaaaaaa gcttaacgag gacgggaaaa 1434

aaattctccc gtccttattc cgttttcccg tttcttacat acaataaacc aatcaactaa 1494

accgctgaat taggtgatgc tgtgaaaaaa ctgaaaaaac aagtcaaaca cgtcgatttc 1554

gcaaaattcg gcctgtcaga ctatacctct cttctcagaa gaagaagcga aaaaatcatt 1614

aaaacgctga acagaagaaa aaacaaaccg tgaagcttgg actttcaccc tccttctctg 1674

ctgagaaggg gggttatttt catgtctaca ggagcatcat aaaggatgcc cctgtccgcc 1734

ttctcctaca gat 1747

<210> 75
<211> 248
<212> PRT
<213> Bacillus licheniformis

<400> 75

Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu Ile Val Leu Ala Leu
1 5 10 15

Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu Lys Gln Leu Ala Glu
20 25 30

Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu Leu Tyr Val Ile Gly
35 40 45

Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser Ile Phe Thr Asn Pro
50 55 60

Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr Leu Thr Asp Ala Phe
65 70 75 80

Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly Ser Ser Glu Leu Ala
85 90 95

Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn Asp Leu Leu His Thr
100 105 110

Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu Leu Lys Asn Glu Pro
115 120 125

10295.204.ST25.txt

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Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr Ala Glu Gly Ile Glu
    130                 135                 140

Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn Ile Ser Ala Ala Leu
145                 150                 155                 160

Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His Leu Leu Glu His Met
                165                 170                 175

Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp Arg Lys Asp Val Tyr
            180                 185                 190

Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro Phe Ser Ile His Asp
        195                 200                 205

Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp Leu Val Thr Glu Phe
    210                 215                 220

Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile Tyr Asp Leu Leu Leu
225                 230                 235                 240

Pro Asn Glu Glu Glu Gly Asp Asp
                245

<210>  76
<211>  2020
<212>  DNA
<213>  Bacillus licheniformis

<220>
<221>  CDS
<222>  (501)..(1742)

<400>  76
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agttgagtta gaggaattaa aaacgaagag aaaagaactt ataaattgga ggctaaaaga     120

tattatttca gaagagattt taaaagagga aatggaagat ttacgagagg aagaaaaatt     180

aataataact cgaattgaaa aattacagca cctcattaaa ctcagagata aaaccttttt     240

aaccaatatc atttcaactt cactacacga tctaaagaac tttttcaata ttatcgaaga     300

tgatgacaaa aaggaattac ttcgttctct cattgaagag attcacgtaa atccaggaaa     360

aactactaag gatagaacga tcaaagaagt gatttataag tttgatttaa aatatttgaa     420

atcaattgaa ctaagagaag gggaacatct tttctctttt ttgtgtttca tattataatt     480

acaaggaagg gaggattatt atg cac gaa ata aaa cgt gtc gca att tac tgt     533
                      Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys
                      1               5                   10

aga gtt tct acc gaa gag cag gca acg gaa gga tac agc ata tct gcc      581
Arg Val Ser Thr Glu Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala
            15                  20                  25
```

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caa tta caa act tta cgt caa tat act cag tta tat ggt tgg gag att      629
Gln Leu Gln Thr Leu Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile
    30                  35                  40

gca gag gaa tat gta gat gag gga ata agt gga aag aac att agc ggt      677
Ala Glu Glu Tyr Val Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly
45                  50                  55

cgc cct gca atg caa aaa ctt att tca gat gtt gaa aag gat aaa ttt      725
Arg Pro Ala Met Gln Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe
60                  65                  70                  75

caa gct gtt ctt gtt tgg aag atc tca cgc cta tca cga aat atg tta      773
Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu
                80                  85                  90

gat act ctc act cta tta gac aaa ttc gaa gat tat gga gta aag ttc      821
Asp Thr Leu Thr Leu Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe
            95                  100                 105

atc tct tac tct gaa aac ttt gat aca ggc agt cca att ggt cgt tta      869
Ile Ser Tyr Ser Glu Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu
        110                 115                 120

gtt gtt caa cta atg gct tcc att gca gaa atg gag cgt aat acg tta      917
Val Val Gln Leu Met Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu
    125                 130                 135

tct gag aac gtt aag ctc gga atg aaa cag aga gca tta gaa ggt tca      965
Ser Glu Asn Val Lys Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser
140                 145                 150                 155

tgg aat gga ggc gtt gta ttt ggc tac gat aca att gaa aaa gag ctt     1013
Trp Asn Gly Gly Val Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu
                160                 165                 170

gtg atc aac aaa aag gaa gct gag att gta caa caa atc tat caa cta     1061
Val Ile Asn Lys Lys Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu
            175                 180                 185

tat gcc aat ggt aaa ggc tta aag tca atc gca aac tac tta aat aaa     1109
Tyr Ala Asn Gly Lys Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys
        190                 195                 200

gca ggt tac aga act aaa cgg aat tgt tat ttt tcg ata aac ggt gta     1157
Ala Gly Tyr Arg Thr Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val
    205                 210                 215

gct caa atc tta gac aat gtt atc tat aac ggg aag atc agt tgg tta     1205
Ala Gln Ile Leu Asp Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu
220                 225                 230                 235

aaa gtt gaa aat tgg gat aca aaa cgg agg aga ggg aaa aat cca aat     1253
Lys Val Glu Asn Trp Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn
                240                 245                 250

cct atc ctt gta gaa gga cag cat gaa gcc att att tcc gat gaa tta     1301
Pro Ile Leu Val Glu Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu
            255                 260                 265

tgg agt atg gta caa gca agg cgg aaa agt aaa tca ttt aaa caa agg     1349
Trp Ser Met Val Gln Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg
        270                 275                 280

caa tct aat gaa cca ttt tta ctt agc agt ctt tta cgt tgc ccc gat     1397
Gln Ser Asn Glu Pro Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp
    285                 290                 295
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tgt ggt caa ggt atg gtt cct gcc att aca aca aat aaa cga aag gat      1445
Cys Gly Gln Gly Met Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp
300                 305                 310                 315

gga aca aag aag aaa tat cgt tat tat gtt tgc tct aac ttt cat aac      1493
Gly Thr Lys Lys Lys Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn
                320                 325                 330

aaa ggt tca tct gca tgt aga gca aat tca ata aaa gca tat gat gca      1541
Lys Gly Ser Ser Ala Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala
            335                 340                 345

gaa tac gaa gta att aat aag att gag aag atc ctt tcc aac caa aat      1589
Glu Tyr Glu Val Ile Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn
        350                 355                 360

cag tta ttc tct aaa ctt caa tct ata aat act act tcg att gaa tct      1637
Gln Leu Phe Ser Lys Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser
    365                 370                 375

tta aac caa ctc aat agt gaa ttg aaa caa tta gaa aat cgc cta tca      1685
Leu Asn Gln Leu Asn Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser
380                 385                 390                 395

gaa ata caa gag tac aga atc gtt act tgg aag cat ttg agc aaa aga      1733
Glu Ile Gln Glu Tyr Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg
                400                 405                 410

cct tac caa tagcaatctt gcaagaacga ttacagcatg tctctaaaga              1782
Pro Tyr Gln

aaaagcagag ttagaacaaa ggcacaatga atcactgggc aattaagctc gaacgatgca    1842

aaagtaataa aaccagaact gattcaaaag ctttagaaaa aattccttta gtctataaac    1902

atcatcaaga gaaagcaaaa cagttactca acttttgctt ataaattaca gtaagcatca    1962

atgggtcatc acgattgtcg atcaattgaa ctcgactttg actttcagaa gtcatatt      2020


<210>  77
<211>  414
<212>  PRT
<213>  Bacillus licheniformis

<400>  77

Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys Arg Val Ser Thr Glu
1               5                   10                  15

Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala Gln Leu Gln Thr Leu
            20                  25                  30

Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile Ala Glu Glu Tyr Val
        35                  40                  45

Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly Arg Pro Ala Met Gln
    50                  55                  60

Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe Gln Ala Val Leu Val
65                  70                  75                  80
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Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu Asp Thr Leu Thr Leu
85 90 95

Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe Ile Ser Tyr Ser Glu
100 105 110

Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu Val Val Gln Leu Met
115 120 125

Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu Ser Glu Asn Val Lys
130 135 140

Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser Trp Asn Gly Gly Val
145 150 155 160

Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu Val Ile Asn Lys Lys
165 170 175

Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu Tyr Ala Asn Gly Lys
180 185 190

Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys Ala Gly Tyr Arg Thr
195 200 205

Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val Ala Gln Ile Leu Asp
210 215 220

Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu Lys Val Glu Asn Trp
225 230 235 240

Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn Pro Ile Leu Val Glu
245 250 255

Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu Trp Ser Met Val Gln
260 265 270

Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg Gln Ser Asn Glu Pro
275 280 285

Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp Cys Gly Gln Gly Met
290 295 300

Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp Gly Thr Lys Lys Lys
305 310 315 320

Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn Lys Gly Ser Ser Ala
325 330 335

Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala Glu Tyr Glu Val Ile
340 345 350

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Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn Gln Leu Phe Ser Lys
        355                 360                 365

Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser Leu Asn Gln Leu Asn
    370                 375                 380

Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser Glu Ile Gln Glu Tyr
385                 390                 395                 400

Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg Pro Tyr Gln
                405                 410


&lt;210&gt;  78
&lt;211&gt;  1417
&lt;212&gt;  DNA
&lt;213&gt;  Bacillus licheniformis


&lt;220&gt;
&lt;221&gt;  CDS
&lt;222&gt;  (510)..(1298)

&lt;400&gt;  78
tgcggacatc cgcttgcttt tctcccgctt ttgaaaccgt ttcttccggc gcaccccatc      60

ctgaatgaat cagggtaaat tcggtttttt ctgcagaaag ctctttcaat tcaaatgtga     120

cgatccatcc cgacgtatcc cagctgaaag cgagtcgatg cggcgcatca agctcgatca     180

ctttgcacgg ggaggggccg aaaggagact gcagggtgaa ttcgcagccg atctccgggc     240

ggaaatcatt aggcataaac caggcggcga tgccttcact ggtggcgacg gcctcccaca     300

ctttttctat cgatgcgtga aaaacagcct gtttatgtat atcaggcact agttgattgc     360

tcataataga cctcctagaa aaaagtaaaa ccaaatggtt tcctttctat tatatgaaac     420

cttttagttt tatgtcaatg ttccgtcata attccctggg acaaggcata tcattgaaca     480

aacgaacctg aatgtaaagg atgagggtt atg agt cat aga gca gat gag att     533
                                Met Ser His Arg Ala Asp Glu Ile
                                1               5

cga aaa aga atg gcc agg aaa aga aag cgg aaa aca ccg gac aaa cag     581
Arg Lys Arg Met Ala Arg Lys Arg Lys Arg Lys Thr Pro Asp Lys Gln
    10                  15                  20

ccc ttt tca tca gac ggc aaa aag cgg ccg ctc aag ccg cct gca tgg     629
Pro Phe Ser Ser Asp Gly Lys Lys Arg Pro Leu Lys Pro Pro Ala Trp
25                  30                  35                  40

aca gcc ttt tcg gaa gat gaa aaa gga gga gac ttc cct ccg cct gaa     677
Thr Ala Phe Ser Glu Asp Glu Lys Gly Gly Asp Phe Pro Pro Pro Glu
                45                  50                  55

gga agt tcc ctg ctg ata aac ggg aag cac ccg ctt gtc aag gcg gat     725
Gly Ser Ser Leu Leu Ile Asn Gly Lys His Pro Leu Val Lys Ala Asp
            60                  65                  70

gcg ctc atc ttg aaa tgt ctt ctg tcg gca tgc ctt gtt ctt gtg tcc     773
Ala Leu Ile Leu Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser
        75                  80                  85

gcc att gcc tac aaa ggc cag ttt gaa ccc gca aac caa atc aaa ccg     821
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Ala Ile Ala Tyr Lys Gly Gln Phe Glu Pro Ala Asn Gln Ile Lys Pro
90 95 100

gtt atc agc cag gtg ttt act gaa gag ttc caa ttt gcg gcc ctc cag 869
Val Ile Ser Gln Val Phe Thr Glu Glu Phe Gln Phe Ala Ala Leu Gln
105 110 115 120

aat tgg tat gaa tcc aag ttc ggc gat ccc ctc gca ttc ttt cag ccg 917
Asn Trp Tyr Glu Ser Lys Phe Gly Asp Pro Leu Ala Phe Phe Gln Pro
125 130 135

aaa ggc gcc aaa ccg tcc ggc cag gtc gag gtg aat cag gat ctc gct 965
Lys Gly Ala Lys Pro Ser Gly Gln Val Glu Val Asn Gln Asp Leu Ala
140 145 150

gta cct gcc gta gga aag gtt cag gag aaa ttc tca ggg cag ggc att 1013
Val Pro Ala Val Gly Lys Val Gln Glu Lys Phe Ser Gly Gln Gly Ile
155 160 165

aag gta gaa aca gaa gac gaa acg atc cgc agc atg aag gaa ggc tat 1061
Lys Val Glu Thr Glu Asp Glu Thr Ile Arg Ser Met Lys Glu Gly Tyr
170 175 180

gtc att gaa gtg gac aaa aat ccg gaa aca ggc ctg acg gtg gtc ttg 1109
Val Ile Glu Val Asp Lys Asn Pro Glu Thr Gly Leu Thr Val Val Leu
185 190 195 200

cag cat gcg gac aac agc tat acc tac tac ggc cag ctg aaa aaa gcg 1157
Gln His Ala Asp Asn Ser Tyr Thr Tyr Tyr Gly Gln Leu Lys Lys Ala
205 210 215

gat gtc gct tta tac gat tat ata gat aaa gga acg aag ctc gga acg 1205
Asp Val Ala Leu Tyr Asp Tyr Ile Asp Lys Gly Thr Lys Leu Gly Thr
220 225 230

att gag cag gat aaa aat caa aaa ggc atc tat tac ttt gcg atc aaa 1253
Ile Glu Gln Asp Lys Asn Gln Lys Gly Ile Tyr Tyr Phe Ala Ile Lys
235 240 245

caa gga gag gaa ttt gtt gat ccg ata cag gtg atc aca ttt gag 1298
Gln Gly Glu Glu Phe Val Asp Pro Ile Gln Val Ile Thr Phe Glu
250 255 260

taaatggacg gagctcttca ccaagcttca cattcatccg ctgctgtggc ttgtcatggc 1358

gatcggtatc atgacaggac atattaaagg cgcgtgtttt gtttaatgca cccaggaag 1417

<210> 79
<211> 263
<212> PRT
<213> Bacillus licheniformis

<400> 79

Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg Met Ala Arg Lys Arg
1 5 10 15

Lys Arg Lys Thr Pro Asp Lys Gln Pro Phe Ser Ser Asp Gly Lys Lys
20 25 30

Arg Pro Leu Lys Pro Pro Ala Trp Thr Ala Phe Ser Glu Asp Glu Lys
35 40 45

Gly Gly Asp Phe Pro Pro Pro Glu Gly Ser Ser Leu Leu Ile Asn Gly

50 55 60

Lys His Pro Leu Val Lys Ala Asp Ala Leu Ile Leu Lys Cys Leu Leu
65 70 75 80

Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Gly Gln Phe
85 90 95

Glu Pro Ala Asn Gln Ile Lys Pro Val Ile Ser Gln Val Phe Thr Glu
100 105 110

Glu Phe Gln Phe Ala Ala Leu Gln Asn Trp Tyr Glu Ser Lys Phe Gly
115 120 125

Asp Pro Leu Ala Phe Phe Gln Pro Lys Gly Ala Lys Pro Ser Gly Gln
130 135 140

Val Glu Val Asn Gln Asp Leu Ala Val Pro Ala Val Gly Lys Val Gln
145 150 155 160

Glu Lys Phe Ser Gly Gln Gly Ile Lys Val Glu Thr Glu Asp Glu Thr
165 170 175

Ile Arg Ser Met Lys Glu Gly Tyr Val Ile Glu Val Asp Lys Asn Pro
180 185 190

Glu Thr Gly Leu Thr Val Val Leu Gln His Ala Asp Asn Ser Tyr Thr
195 200 205

Tyr Tyr Gly Gln Leu Lys Lys Ala Asp Val Ala Leu Tyr Asp Tyr Ile
210 215 220

Asp Lys Gly Thr Lys Leu Gly Thr Ile Glu Gln Asp Lys Asn Gln Lys
225 230 235 240

Gly Ile Tyr Tyr Phe Ala Ile Lys Gln Gly Glu Glu Phe Val Asp Pro
245 250 255

Ile Gln Val Ile Thr Phe Glu
260

<210> 80
<211> 1468
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (982)..(1428)

<400> 80
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tgaagctgta cataaatcgt ttcctgacct tgatgtccaa accgtcggcg gttctgaaac    180
catcgtggag atccaatatc cgaaaaggga tctgtcgccc gtgcttttca tcgccgtctg    240
gctgctcttg ttcgtcggtg ccggccttgc cgtcatgaac tttcatgaag atgtcagcat    300
gagggaagtg cacatcctgc tttacgaaat ggtgacgggc aaggtgaacc gctatccata    360
ccttttgcag gttccgtaca gcatcggtct tggcctcggc atgatcttgt tttttaatca    420
tttatttaaa aaacggttta acgaggagcc cagccccctg gaggtcgaga tgtttaaata    480
tcagcttgat ttggaccatt atgtggccat gcacgaaaac aaagaaacga caaaggatat    540
tcatgatcat tagcgtgata tttatcatct ttctcggact cgcaggaggg gttgctgttg    600
gatccggctt tgtcgctttt cttaccgtgc ttggcattat cccgaggctg actcagctga    660
cgaaaacaaa aggatttatc caggcgtatg aatgggctgt cattttaggc gcggttttcg    720
gaggatggga atcgctgaac atgtcccgct tttttttatc caaatggctg cttgttccga    780
tcggcctttt tgcgggcgtt ttcattggaa tgcttgcagc ggcgctaaca gaagtcttga    840
acgtgctgcc gatactggcg aaacgcatcg ggatgggaga ccggattttg atactttttaa    900
tggccattgt tttcggcaag attctcggat cgatgttcca atggctcatt tttgttcatt    960
tgtcataaaa ggaggattat g atg tca agt ttg aaa gat aat tat caa tcg     1011
                        Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser
                        1               5                   10

aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc     1059
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile
                15                  20                  25

aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc     1107
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe
            30                  35                  40

cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg     1155
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly
        45                  50                  55

aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc     1203
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly
    60                  65                  70

ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc     1251
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala
75                  80                  85                  90

gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag     1299
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu
                95                 100                 105

cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag     1347
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys
            110                 115                 120

ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg     1395
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val
        125                 130                 135

ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa   1448
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe
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140 145

attaacagga aaacaaacat 1468

<210> 81
<211> 149
<212> PRT
<213> Bacillus licheniformis

<400> 81

Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
1 5 10 15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
130 135 140

Phe Asp Lys Leu Phe
145

<210> 82
<211> 1453
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (504)..(950)

<400> 82
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tggatccggc tttgtcgctt ttcttaccgt gcttggcatt atcccgaggc tgactcagct 180

gacgaaaaca aaaggattta tccaggcgta tgaatgggct gtcattttag gcgcggtttt 240

cggaggatgg gaatcgctga acatgtcccg ctttttttta tccaaatggc tgcttgttcc 300

gatcggcctt tttgcgggcg ttttcattgg aatgcttgca gcggcgctaa cagaagtctt 360

gaacgtgctg ccgatactgg cgaaacgcat cgggatggga gaccggattt tgatactttt 420

aatggccatt gttttcggca agattctcgg atcgatgttc caatggctca tttttgttca 480

tttgtcataa aaggaggatt atg atg tca agt ttg aaa gat aat tat caa tcg 533
Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser
1 5 10

aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc 581
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile
15 20 25

aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc 629
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe
30 35 40

cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg 677
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly
45 50 55

aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc 725
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly
60 65 70

ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc 773
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala
75 80 85 90

gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag 821
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu
95 100 105

cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag 869
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys
110 115 120

ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg 917
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val
125 130 135

ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa 970
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe
140 145

attaacagga aaacaaacat gggaattcga gaacccgctg tttgttaact caagcggaac 1030

agcggtcggt cccaaagaaa aagaaggtcc tcttggacac ttatttgaca aaagctatga 1090

tgaaatgcac tgcaaccaga aaaactggga aatggcagag cgcaagctga tggaggatgc 1150

ggttcagtcc gcgttatcaa aacaaaatct taaaaaggaa gacatcgata tctttttggc 1210

tggcgatctg ctcaaccaaa acgtgacagc caactatgtg gcgcggcatt tgaaaattcc 1270

ttttctctgc ttatttggag catgctcgac atcaatggaa tcgatcgcga tcagttcggc 1330

gttgattgac gggggtttcg caaagcgcgc cctagcggca accagcagcc ataatgctac 1390

ggcagaaagg cagttccgct acccgacgga atacgggggg caaaaaccgg gaaccgcgac 1450

ttc 1453

<210> 83
<211> 149
<212> PRT
<213> Bacillus licheniformis

<400> 83

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Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
1               5                   10                  15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
            20                  25                  30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
        35                  40                  45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
    50                  55                  60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
65                  70                  75                  80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
                85                  90                  95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
            100                 105                 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
        115                 120                 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
    130                 135                 140

Phe Asp Lys Leu Phe
145
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<210> 84
<211> 2020
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1517)

<400> 84

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atcaatcgaa agttaaagcg tatcagcctt caccgcctta tgtcctgaac tgtatcaagg     120
catttctcgt cggtggtctg atttgtacga tcggccaggc tttccagaat ttttatatgg     180
ctgtgttcca ttttgatgaa aaaacggccg ggaacccgac ggttgccacg ctgatcctga     240
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tctccgctct gttaacaggc cttggcgtct acgacagaat cggacagttt gccggcgctg      300
gttctgccgt tccggttaca gggtttgcca acagtatgac gagcgcagcg ctggagcata      360
aaagcgaaag ctacgtcctc ggcgtatgga caaacatgtt caagcttgcg ggaaacgtca      420
tcgtgttcgg tgttgtggcc gcttatattg tggggatgat ccgctttgcc tttgacaagc      480
tgttttagga ggaaaacatc atg aaa tta aca gga aaa caa aca tgg gaa ttc      533
                      Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe
                      1               5                   10

gag aac ccg ctg ttt gtt aac tca agc gga aca gcg gtc ggt ccc aaa        581
Glu Asn Pro Leu Phe Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys
            15                  20                  25

gaa aaa gaa ggt cct ctt gga cac tta ttt gac aaa agc tat gat gaa        629
Glu Lys Glu Gly Pro Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu
        30                  35                  40

atg cac tgc aac cag aaa aac tgg gaa atg gca gag cgc aag ctg atg        677
Met His Cys Asn Gln Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met
    45                  50                  55

gag gat gcg gtt cag tcc gcg tta tca aaa caa aat ctt aaa aag gaa        725
Glu Asp Ala Val Gln Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu
60                  65                  70                  75

gac atc gat atc ttt ttg gct ggc gat ctg ctc aac caa aac gtg aca        773
Asp Ile Asp Ile Phe Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr
                80                  85                  90

gcc aac tat gtg gcg cgg cat ttg aaa att cct ttt ctc tgc tta ttt        821
Ala Asn Tyr Val Ala Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe
            95                  100                 105

gga gca tgc tcg aca tca atg gaa tcg atc gcg atc agt tcg gcg ttg        869
Gly Ala Cys Ser Thr Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu
        110                 115                 120

att gac ggg ggt ttc gca aag cgc gcc cta gcg gca acc agc agc cat        917
Ile Asp Gly Gly Phe Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His
    125                 130                 135

aat gct acg gca gaa agg cag ttc cgc tac ccg acg gaa tac ggg ggg        965
Asn Ala Thr Ala Glu Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly
140                 145                 150                 155

caa aaa ccg gga acc gcg act tcg aca gtg acc gga agc gga gcg gtc       1013
Gln Lys Pro Gly Thr Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val
                160                 165                 170

gtc ctc agc cag cag ccc ggc gga att aaa att aca agc gca act gtc       1061
Val Leu Ser Gln Gln Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val
            175                 180                 185

gga agg gtt atc gac ttg ggg att acc gat tcg caa gat atg ggg tcg       1109
Gly Arg Val Ile Asp Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser
        190                 195                 200

gcg atg gca ccc gct gct gcg gat acg atc aag cag cat ttg gag gat       1157
Ala Met Ala Pro Ala Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp
    205                 210                 215

ctg gga cgc acc cct gat gat tac gat ctg atc tta acc ggc gac ctt       1205
Leu Gly Arg Thr Pro Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu
220                 225                 230                 235
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tca ggc gtc ggc agc ccg att ttg aag gat ctg tta aaa gag gaa gga      1253
Ser Gly Val Gly Ser Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly
                240                 245                 250

atc aat gtc ggg aca aaa cat aat gac tgc ggg ctg atg atc tat acg      1301
Ile Asn Val Gly Thr Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr
            255                 260                 265

cct gac cag caa gtt ttt gca ggt gga agc gga tgc gct tgt tcc gcg      1349
Pro Asp Gln Gln Val Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala
        270                 275                 280

gtc gtc acc ttt gcc cat att ttc aaa gaa att gaa gcg gga agg ctg      1397
Val Val Thr Phe Ala His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu
    285                 290                 295

aac aga gtg ctt gtt gtc gcg aca ggc gcc ctt tta agc ccg acg atc      1445
Asn Arg Val Leu Val Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile
300                 305                 310                 315

atc cag caa aaa gaa tcg ata cca tgc att gcc cat ggc gtc gta ttt      1493
Ile Gln Gln Lys Glu Ser Ile Pro Cys Ile Ala His Gly Val Val Phe
                320                 325                 330

gaa cgg gcc gaa agg ggg aac gct taagatggag tatgtcattg cttttattgc     1547
Glu Arg Ala Glu Arg Gly Asn Ala
            335

aggcgggctg atttgcgtca tcggacagct cttgcttgat atcttcaaaa tgacgccggc    1607

tcatgtcatg tcaacttttg tcgtatctgg agcgatcctt gacggattcg gcatttacga    1667

ccgttttatc gaatttgccg gtgccggggc tacagtcccg attgtcagct tcggccactc    1727

tcttttgcac ggcgcgatgc accaggctga gaaacatggc tttatcggaa tcggcatggg    1787

gatatttgaa ctgacatctg ccggtatatc tgccgctatc ttgttcgctt ttcttgttgc    1847

cgtgattttt aaaccgaaag gataaaggaa aatgccagca aaacgcaagg tcattttggt    1907

cacagacggc gatatatacg ctgcaaaagc aatcgaatat gcagcaagaa aaacgggtgg    1967

ccgctgcatt tcccaatcgg cggggaatcc gagcgttaaa acaggaccgg agc           2020


<210>  85
<211>  339
<212>  PRT
<213>  Bacillus licheniformis

<400>  85

Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe Glu Asn Pro Leu Phe
1               5                   10                  15

Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys Glu Lys Glu Gly Pro
            20                  25                  30

Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu Met His Cys Asn Gln
        35                  40                  45

Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met Glu Asp Ala Val Gln
    50                  55                  60
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Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu Asp Ile Asp Ile Phe
65 70 75 80

Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr Ala Asn Tyr Val Ala
85 90 95

Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe Gly Ala Cys Ser Thr
100 105 110

Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu Ile Asp Gly Gly Phe
115 120 125

Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His Asn Ala Thr Ala Glu
130 135 140

Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly Gln Lys Pro Gly Thr
145 150 155 160

Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val Val Leu Ser Gln Gln
165 170 175

Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val Gly Arg Val Ile Asp
180 185 190

Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser Ala Met Ala Pro Ala
195 200 205

Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp Leu Gly Arg Thr Pro
210 215 220

Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu Ser Gly Val Gly Ser
225 230 235 240

Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly Ile Asn Val Gly Thr
245 250 255

Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr Pro Asp Gln Gln Val
260 265 270

Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala Val Val Thr Phe Ala
275 280 285

His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu Asn Arg Val Leu Val
290 295 300

Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile Ile Gln Gln Lys Glu
305 310 315 320

Ser Ile Pro Cys Ile Ala His Gly Val Val Phe Glu Arg Ala Glu Arg
325 330 335

Gly Asn Ala

<210> 86
<211> 2473
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1970)

<400> 86
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cgtcatgttt gatgattccg gacttcaagg tgaaggcccg ggagagacag ctatgaaata     180

tgtagcgatg catcccgata tcgaggtgct cggagtcatc gccgtcgctt caaaaactca     240

ttatgcagag tggacgagag tcgatgtatc aatcgatgca gaaggcgaac tgacagagta     300

cggcgtcgat aaacacgggg tcaaagagtt cgatgtcaaa cgaatgaatg gtgatacagt     360

ctattgcctt gaccagctgg atgttccgat cattgtcgga atcggtgata tcggtaagat     420

gaacagaaaa gacgatgtgg aaaaaggttc gccgattaca atgaaagcgg tcgagctcat     480

tttagaaagg agcgggtatc atg agt gct caa aag caa gag aag acg aac gta     533
                      Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val
                      1               5                   10

ttc ctt gat cct tct aag aat gaa gcg tat ttc aag aag cgg gtc ggc       581
Phe Leu Asp Pro Ser Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly
            15                  20                  25

atg gga gaa agc ttt gac ctt ggc gta cgg aag gtc ttt att ctc gga       629
Met Gly Glu Ser Phe Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly
        30                  35                  40

cat gaa gtt cag ctt tat tat gtc aac gga ttg tgc gac aca caa tac       677
His Glu Val Gln Leu Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr
    45                  50                  55

atc att cac ctg tta aga gaa ctg gtg cat ctg aat gat aaa gaa aaa       725
Ile Ile His Leu Leu Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys
60                  65                  70                  75

gaa tcg ggc gag gtc gaa gac atc gtc gaa aac agg ctt ttg aac cag       773
Glu Ser Gly Glu Val Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln
                80                  85                  90

cag gtt tca aaa gcg gaa acg ctt gat gaa gct gtc gac caa gtg ttg       821
Gln Val Ser Lys Ala Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu
            95                  100                 105

tca gga ctg gtt gcc atc atc gtc gaa gat gcg ggc ttt gct ttt atc       869
Ser Gly Leu Val Ala Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile
        110                 115                 120

atc gat gtc aga agc tac ccg ggc aga acg ccg gaa gaa cct gat aca       917
Ile Asp Val Arg Ser Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr
    125                 130                 135

gaa aaa gtc gta cgc ggt gca agg gac gga ctc gtc gag aac atc atc       965
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Glu Lys Val Val Arg Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile
140 145 150 155

gtc aac aca gcc ctg att aga cgc cgg atc aga gat gag cgc ttg cgc 1013
Val Asn Thr Ala Leu Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg
160 165 170

tac aaa atg ctt cat atc ggt gaa cgc tct aaa aca gac atc tgc ctc 1061
Tyr Lys Met Leu His Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu
175 180 185

tgc tat ttg gaa gac gtt gca gat ccc gat ctt gtt gaa gta tta aaa 1109
Cys Tyr Leu Glu Asp Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys
190 195 200

aaa gaa att gaa gat gtg aag atc gac ggg ctg ccg atg tcg gat aaa 1157
Lys Glu Ile Glu Asp Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys
205 210 215

tcg gta gag gaa ttc ctg gtc ggc caa ggc tac aat ccg ttt ccg ctt 1205
Ser Val Glu Glu Phe Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu
220 225 230 235

gtc agg ttt acg gaa agg gca gac gta gcc gca agc cat att tta gag 1253
Val Arg Phe Thr Glu Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu
240 245 250

ggg cat gtc atc gtg atc gtc gat acg tcg cca agc gtc atc atc aca 1301
Gly His Val Ile Val Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr
255 260 265

ccg acc act ttg ttt cac cat gtt cag cat gct gag gaa tac aga cag 1349
Pro Thr Thr Leu Phe His His Val Gln His Ala Glu Glu Tyr Arg Gln
270 275 280

acg ccg gct gtt ggg acg ttt tta agg tgg gtg cgg ttt ttc ggt att 1397
Thr Pro Ala Val Gly Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile
285 290 295

ttg gcc tcc acc ttt ttg ctg ccg ctt tgg ctg ctg ttt gtc att cat 1445
Leu Ala Ser Thr Phe Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His
300 305 310 315

ccg tcg ctc ttg cct gat aat tta tcg ttt atc ggg ttg aat aaa gac 1493
Pro Ser Leu Leu Pro Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp
320 325 330

acc cat att ccg att atc atg cag att ttc ctg gcg gat ctc ggc gtc 1541
Thr His Ile Pro Ile Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val
335 340 345

gaa ttt tta aga atg gcc gcc att cat acg ccg acg gcg ctt tcg act 1589
Glu Phe Leu Arg Met Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr
350 355 360

gca atg ggc ctg atc gcc gct gta ttg atc ggc gat atc gcg atc aat 1637
Ala Met Gly Leu Ile Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn
365 370 375

gtc ggc ttg ttt tct ccc gaa gtc att tta tac gtt tcc ctc tcg gca 1685
Val Gly Leu Phe Ser Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala
380 385 390 395

atc gga gcc tac acg aca cca agc tac gag ctg agc ctg gcg aat aaa 1733
Ile Gly Ala Tyr Thr Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys
400 405 410

atg gtg aag ctg ttt atg ctg ata ttg gtg gcg ctt ttt aaa gtg gag 1781

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Met Val Lys Leu Phe Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu
            415                 420                 425

gga ttt gtc atc gga tta acg atc tta act ata gtg atg act tcg atc      1829
Gly Phe Val Ile Gly Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile
        430                 435                 440

agg tca ttg cga acg cct tac tta tgg cct ctc ctc ccg ttc aat gga      1877
Arg Ser Leu Arg Thr Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly
    445                 450                 455

aaa gcg ttt tgg cat gtt ctc gtg cgc acg tcc gtt cca ggg gga aaa      1925
Lys Ala Phe Trp His Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys
460                 465                 470                 475

gtc agg ccg agc atc gtt cat ccg aga aac cgc tcc aga cag ccg          1970
Val Arg Pro Ser Ile Val His Pro Arg Asn Arg Ser Arg Gln Pro
                480                 485                 490

tgaagccggc attcgaagag gcttttcccc ggggaaaagc ctctttttca ataatcgaat    2030

tccggtcttt gagtaccgat gcctctgtat tcattggcag agatcgcgac tgcccggagg    2090

ctgcagatgt tgttctgtct tctgatcgga tagacgacat acagcatttc gcggccgtac    2150

gggtcaatcg ttgacgaatg aaggaaaacc tcagttcctc tccgccaaaa tctcgtattc    2210

gccggagctg taataatctg cccttcataa ggctcataaa ttctctgttc ataatgcgca    2270

gccggctgat aaggggcgta tacatcttca ggtgcatagc cgggagcggg ggtgtaggga    2330

taacgatttg gatacatatg ataacctctt tcccacttcg tttttggtt ttcatcttta     2390

agattatatt caggtaaatg cctatttgta tgggcgaaaa tctcagcttt tcggctcttt    2450

ttttattgaa tggacgttgt gta                                            2473

<210>  87
<211>  490
<212>  PRT
<213>  Bacillus licheniformis

<400>  87

Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val Phe Leu Asp Pro Ser
1               5                   10                  15

Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly Met Gly Glu Ser Phe
            20                  25                  30

Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly His Glu Val Gln Leu
        35                  40                  45

Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr Ile Ile His Leu Leu
    50                  55                  60

Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys Glu Ser Gly Glu Val
65                  70                  75                  80

Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln Gln Val Ser Lys Ala
                85                  90                  95
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Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu Ser Gly Leu Val Ala
100 105 110

Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile Ile Asp Val Arg Ser
115 120 125

Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr Glu Lys Val Val Arg
130 135 140

Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile Val Asn Thr Ala Leu
145 150 155 160

Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg Tyr Lys Met Leu His
165 170 175

Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu Cys Tyr Leu Glu Asp
180 185 190

Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys Lys Glu Ile Glu Asp
195 200 205

Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys Ser Val Glu Glu Phe
210 215 220

Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu Val Arg Phe Thr Glu
225 230 235 240

Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu Gly His Val Ile Val
245 250 255

Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr Pro Thr Thr Leu Phe
260 265 270

His His Val Gln His Ala Glu Glu Tyr Arg Gln Thr Pro Ala Val Gly
275 280 285

Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile Leu Ala Ser Thr Phe
290 295 300

Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His Pro Ser Leu Leu Pro
305 310 315 320

Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp Thr His Ile Pro Ile
325 330 335

Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val Glu Phe Leu Arg Met
340 345 350

Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr Ala Met Gly Leu Ile
355 360 365

Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn Val Gly Leu Phe Ser
370 375 380

Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala Ile Gly Ala Tyr Thr
385 390 395 400

Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys Met Val Lys Leu Phe
405 410 415

Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu Gly Phe Val Ile Gly
420 425 430

Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile Arg Ser Leu Arg Thr
435 440 445

Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly Lys Ala Phe Trp His
450 455 460

Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys Val Arg Pro Ser Ile
465 470 475 480

Val His Pro Arg Asn Arg Ser Arg Gln Pro
485 490

<210> 88
<211> 1567
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1064)

<400> 88
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cagccgcttt acgagctgtc tgtcacagca aagccgaaga acattccgca gacgatcgag 180

gttgatattt ccagtctcga agtcaatgat gttctaaccg tcggcgatat tccgaccaaa 240

ggcgattatt catacaacca tgagcctgat gaagttgttg catccattct tcctcctcaa 300

aagcaggaag aaacagaagc cgaatcagct gctcaagacg ttgaggaacc agaaaaaggc 360

actgaagagg aaaaagaaga ataaatacgt aagacgtaat ccgcccgcgg ttacgtcttt 420

tgtgctagaa tgaggggaaa ttaggatgct ccccctcagt atgctgaggc agggttttgc 480

ttaagggagg atatagaata atg ctt gtg ttt gca gga ttg ggc aat ccg ggt 533
Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly
1 5 10

aaa aca tat gaa aat acg aga cac aat gta ggt ttt atg acg att gac 581
Lys Thr Tyr Glu Asn Thr Arg His Asn Val Gly Phe Met Thr Ile Asp
15 20 25

gag ctc tcg aaa gag tgg aac att ccg ctt gat aaa aca aag ttc aac 629
Glu Leu Ser Lys Glu Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn
30 35 40

gga caa tac gga atc ggg ttt gtt tcc ggc aaa aag gtt cta ctt gtt 677
Gly Gln Tyr Gly Ile Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val
45 50 55

aag ccg ctt aca tat atg aat tta tcg gga gaa tgt ttg agg ccg ctt 725
Lys Pro Leu Thr Tyr Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu
60 65 70 75

ttg gac tat tac gag atc cct gtt gac aat ttg aaa gtg att tac gat 773
Leu Asp Tyr Tyr Glu Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp
80 85 90

gat ttg gat ctt ccg acc gga aga atc cgt ctg agg acg aaa gga agc 821
Asp Leu Asp Leu Pro Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser
95 100 105

gca gga ggc cat aac ggc atc aaa tcg acg att cag cat ctg gga aca 869
Ala Gly Gly His Asn Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr
110 115 120

agt gag ttt aac cgg atc aga atc gga ata ggc cgt ccg gta aac ggc 917
Ser Glu Phe Asn Arg Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly
125 130 135

atg aaa gtc gtc gat tat gtg ctt ggc gct ttt aca gat gaa gaa gag 965
Met Lys Val Val Asp Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu
140 145 150 155

ccg gcg ata aaa gag gcc gtc aga caa tcg gcc aag gcc tgt gaa gct 1013
Pro Ala Ile Lys Glu Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala
160 165 170

tct ttg gaa aaa cct ttt tta gaa gtc atg aat gaa ttt aac gca aag 1061
Ser Leu Glu Lys Pro Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys
175 180 185

gta taaggcaaaa gggaacggaa catactagtc ttaaaaagac tcggtatgga 1114
Val

ggttccttta tggctttaca ttattattgc cggcattgcg gcgttaaagt cggaagtctt 1174
gaccattctt atgtaaacag tgaacagtta ggctttaacc acttaacaaa tgatgaaaga 1234
aacgatatga tttcttatat ggataatggg gatttacacg tgaagacgat atgtgaagat 1294
tgtcaagaag cgcttgagcg aaacccggat tatcaccaat atcattcatt tattcaatag 1354
atagctttgg tgtagagact agaccaaagc atttttctat ttgaggaaga gaggaggggc 1414
tcatttgaac aatattcaat cctatataac aaaaagcgat gattttaaat ccatcgtcaa 1474
cggcttgaac gaagggctga aggaacagct gcttgcgggg ctctccggat ctgcccggtc 1534
gttatttaca gccgctctta caaaagaaac gag 1567

<210> 89
<211> 188
<212> PRT
<213> Bacillus licheniformis

<400> 89

Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly Lys Thr Tyr Glu Asn
1 5 10 15

Thr Arg His Asn Val Gly Phe Met Thr Ile Asp Glu Leu Ser Lys Glu
20 25 30

Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn Gly Gln Tyr Gly Ile
35 40 45

Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val Lys Pro Leu Thr Tyr
50 55 60

Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu Leu Asp Tyr Tyr Glu
65 70 75 80

Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp Asp Leu Asp Leu Pro
85 90 95

Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser Ala Gly Gly His Asn
100 105 110

Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr Ser Glu Phe Asn Arg
115 120 125

Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly Met Lys Val Val Asp
130 135 140

Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu Pro Ala Ile Lys Glu
145 150 155 160

Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala Ser Leu Glu Lys Pro
165 170 175

Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys Val
180 185

<210> 90
<211> 2097
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1598)

<400> 90
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aaacagactg ttttacaatg acagcaaagc gacaaacatt cttgcgacga aaaaagcgct 120

gtccgccttt caaaagccgg tcattttgct ggcagggggg cttgaccgcg gaaatgaatt 180

tgatgaacta aagccgcata tgtcttttgt aaaagcggtg atcactttcg gcgagaccgc 240

gccgaagttt gagaagctgg ccgaagaaat gggaatacaa caggttaaac gtgtcgataa 300

tgttgaacaa gcagcaactg cggcgttcag cctgtcagac gaaggagatg tcattcttct 360

gtccccggcc tgcgcaagct gggatcagta caaaacattt gaagaacgtg gtgacatgtt 420

tgtaaacgcc gtgcatatgc ttaaataagg gcttgtctcg taaagatagc cctaagaatt 480

agagcttggg gtgttcggct ttg caa aca aaa aaa acg tca ccg gat ttt ttg 533
Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu
1 5 10

ctg gtt atc att acg cta ttg ctt tta aca atc gga ctg att atg gta 581
Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val
15 20 25

tac agc gcc agt gca gta tgg gcg act tac aaa tac gac gac tcc ttt 629
Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe
30 35 40

ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc atc ggg gtc atc gcc 677
Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala
45 50 55

atg ttt ttc atc atg aac gtc gac tac tgg acg tgg agg act tat gcg 725
Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala
60 65 70 75

aaa ata ctg atc att gta tgt ttc ttt ctg ctc atc atc gtc ctg gtt 773
Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val
80 85 90

ccc ggg atc ggc atg gaa cgg aac ggg tcg agg agc tgg atc gga gtc 821
Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val
95 100 105

ggc gct ttc agc att cag ccg tcc gag ttt atg aaa ctc gcg atg atc 869
Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile
110 115 120

gca ttt ttg gcc aag ttt tta tct gaa aag caa aag aat att acg tcg 917
Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser
125 130 135

ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att gtc ttt tca gct ttt 965
Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe
140 145 150 155

ctg atc atc atg atg cag cct gac ctc gga aca gga acc gtg atg gtc 1013
Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val
160 165 170

ggc aca tgc atc att atg atc ttt gtc gcg ggg gcg aga att tcg cac 1061
Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His
175 180 185

ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt ttt gtc ggc ctt gtg 1109
Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val
190 195 200

ctg tcg gcg ccg tac cgg atc aaa agg atc act tca tac ttg aac cct 1157
Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro
205 210 215

tgg gag gac cct tta gga agc ggc ttt caa atc att cag tct ctt tat 1205
Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr
220 225 230 235

gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc ctc ggc cag agc agg 1253

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Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
                240                 245                 250

caa aag ttt ttc tat ctg cct gag ccg cag aca gat ttt att ttt gcg      1301
Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
            255                 260                 265

att tta tca gag gag ctc ggc ttt atc ggc gga tcg ctg att ctt ttg      1349
Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
        270                 275                 280

ctc ttc agc gtt cta tta tgg aga ggc atc aga atc gcg ctc ggt gcg      1397
Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
    285                 290                 295

ccc gat tta tac ggc agt ttt gtc gcc gtc ggc gtc att tcg atg ata      1445
Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
300                 305                 310                 315

gcg att cag gtt atg atc aat atc gga gtc gtg act ggt ttg att cct      1493
Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
                320                 325                 330

gtt aca ggc att acg ctt ccg ttt tta agc tat ggc ggt tca tca ctg      1541
Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
            335                 340                 345

acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg aat gtc agc agg tat      1589
Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
        350                 355                 360

tct aga tac tagattttgg cgataaccct gttgcgagat agcagggtta              1638
Ser Arg Tyr
    365

tcggcgtgta cataaggatt aagggggaga acagatgcgg attgttgtta gcggaggcgg   1698

aacgggcggc catatttacc ccgcccttgc gtttattaaa gaagtgaaac ggcatcacga   1758

agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata tcgtcgagcg   1818

ggaagggatc cctttcaaag cgattgaaat tacgggtttt aaaagaaaac tttcatttga   1878

aaacgtcaaa accgtcatgc gctttttaaa gggtgtaaaa gaatgcaaag aagaattaaa   1938

acggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc ccgtcgtata   1998

cgccgcttca aaactgggga ttccgacgat tatccacgaa caaaacagcc ttcccggact   2058

caccaataag tttttatcca aatatgttga taaggtagc                           2097
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<210> 91
<211> 366
<212> PRT
<213> Bacillus licheniformis

<400> 91

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Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu Leu Val Ile Ile Thr
1               5                   10                  15

Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val Tyr Ser Ala Ser Ala
            20                  25                  30

Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg
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35 40 45

Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala Met Phe Phe Ile Met
50 55 60

Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile
65 70 75 80

Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val Pro Gly Ile Gly Met
85 90 95

Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile
100 105 110

Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile Ala Phe Leu Ala Lys
115 120 125

Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe
130 135 140

Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe Leu Ile Ile Met Met
145 150 155 160

Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val Gly Thr Cys Ile Ile
165 170 175

Met Ile Phe Val Ala Gly Ala Arg Ile Ser His Phe Val Phe Leu Gly
180 185 190

Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val Leu Ser Ala Pro Tyr
195 200 205

Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu
210 215 220

Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly
225 230 235 240

Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr
245 250 255

Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu
260 265 270

Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu Leu Phe Ser Val Leu
275 280 285

Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly
290 295 300

Ser Phe Val Ala Val Gly Val Ile Ser Met Ile Ala Ile Gln Val Met

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305                 310                 315                 320

Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro Val Thr Gly Ile Thr
                325                 330                 335

Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu Thr Leu Met Leu Met
            340                 345                 350

Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr Ser Arg Tyr
        355                 360                 365


<210>  92
<211>  1882
<212>  DNA
<213>  Bacillus licheniformis


<220>
<221>  CDS
<222>  (501)..(1397)

<400>  92
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atcggttcat acatcataac aaaagggggt ttttttcatg aggctgagtg aactttcggg    120

aaaagaaatc gttgatgtta agcgggccga acggctcggc gtactggggc agacggacct    180

tgagatcaat gagcaggacg gtcagattac cgctcttatc atcccttctg ttaaatggtt    240

cggactagga agaaaacagg ggaatgacat taaggtgccc tggtcgcaaa ttcaaaaaat    300

cggctcggat atgatcattt tggatgttcc ggaaagcagc gtgacaaaag aggagtaagc    360

aaggtggaaa cccgcccgtc ccatgggggc gggctttttg tttttctgga tttcaattca    420

ccgctatttc ctttttgtca tatgatgaaa ttagcttatg aattagatcc ttgtcaaaaa    480

agaaggtgaa tgttagagcc atg tta acc gga ttg acg att gca atc atc ggc    533
                      Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly
                      1               5                   10

ggc gat gca agg cag ctc gag atc atc cgc aag ctg acg gaa cag gat      581
Gly Asp Ala Arg Gln Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp
            15                  20                  25

gca aag gtc ttt tta atc ggt ttt gat cag ctt gat cac ggg ttt acc      629
Ala Lys Val Phe Leu Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr
        30                  35                  40

gga gct aca aaa cta aag ctg aac gaa ctt gat ttt ggc aca ata gac      677
Gly Ala Thr Lys Leu Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp
    45                  50                  55

agc att att ctg cct gta tcg ggc aca tcg atg gaa gga acg gtt gcg      725
Ser Ile Ile Leu Pro Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala
60                  65                  70                  75

act gtt ttt tcc aat gaa aaa gtg gtg tta aaa cag gaa cat tta gaa      773
Thr Val Phe Ser Asn Glu Lys Val Val Leu Lys Gln Glu His Leu Glu
                80                  85                  90

aaa acc aag ccg cac tgc gcg att tat tca ggg att tca aac caa tat      821
Lys Thr Lys Pro His Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr
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                     95                  100                  105
tta gac ggc atg gcc aaa ggg gcg aac cgt cgt ctt atc aag ctc ttt      869
Leu Asp Gly Met Ala Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe
        110                 115                 120

gaa aga gac gat att gcg att tac aac tcg ata cct aca gtc gaa ggt      917
Glu Arg Asp Asp Ile Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly
    125                 130                 135

gcc att atg atg gcc ata cag cat aca gac ttt acg att cac ggc tcg      965
Ala Ile Met Met Ala Ile Gln His Thr Asp Phe Thr Ile His Gly Ser
140                 145                 150                 155

aat gta atg gtt ctc ggg ctg ggg cgg acg gga atg agc atc agc cgg      1013
Asn Val Met Val Leu Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg
                160                 165                 170

acg ttc tcg gcg ctc ggc gca cgc gta aaa gtc gga gct cgc gac tcc      1061
Thr Phe Ser Ala Leu Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser
            175                 180                 185

gcc cac ctc gcc aga atc atg gag atg ggc ctc act cct ttc cac aca      1109
Ala His Leu Ala Arg Ile Met Glu Met Gly Leu Thr Pro Phe His Thr
        190                 195                 200

aac gaa ctt gca gag cat gtt gaa aat atc gac ata tgc atc aat acc      1157
Asn Glu Leu Ala Glu His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr
    205                 210                 215

att cca agc ctg att ctc gat aaa cat gtc ctc tca cga atg aca ccc      1205
Ile Pro Ser Leu Ile Leu Asp Lys His Val Leu Ser Arg Met Thr Pro
220                 225                 230                 235

aga aca tta att ctc gat tta gca acc cgt ccc gga ggc aca gat ttt      1253
Arg Thr Leu Ile Leu Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe
                240                 245                 250

gat ttt gcc gaa aag caa ggc att aaa gcg ctg ctt gct cca gga ctt      1301
Asp Phe Ala Glu Lys Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu
            255                 260                 265

ccc ggg atc gtc gcg cct aaa acg gcg gga cag atc att gcc aat gtt      1349
Pro Gly Ile Val Ala Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val
        270                 275                 280

ttg tgc aac ctt ttg tct gaa tta aca act gac cga aag ggg ctg tca      1397
Leu Cys Asn Leu Leu Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
    285                 290                 295

taatgtcgat caaaggaaaa agaatcggat ttggcctaac gggttcacat tgtacgtatg    1457
atgccgtttt tccgcagatt gaagcgctga tcaacaaagg ggctgaagtc agaccggtcg    1517
tgacgcatac tgtcaagtcg acggatacac gctttggaga aggggaagaa tgggtcagaa    1577
gaatagaaga gctgactgga tttgaagtca ttgattccat tccgaaagct gagcctctcg    1637
ggccgaaaac accgctggac tgcatggttg ttgcgccatt gacgggaaat tcgatgagca    1697
agcttgcaaa cgcccagacg gacagtccgg ttctcatggc ggccaaagcg acgatgagaa    1757
actcccgtcc cgtcgtcctc ggcatttcaa cgaatgacgc gctcggcttg aacggcgtca    1817
acttgatgag gctgatggcg gcaaaaaatg tttactttat tccgttcggc caggatgacc    1877
cttac                                                                1882
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<210> 93
<211> 299
<212> PRT
<213> Bacillus licheniformis

<400> 93

Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly Gly Asp Ala Arg Gln
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Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp Ala Lys Val Phe Leu
            20   25   30

Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr Gly Ala Thr Lys Leu
        35   40   45

Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp Ser Ile Ile Leu Pro
    50   55   60

Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala Thr Val Phe Ser Asn
65   70   75   80

Glu Lys Val Val Leu Lys Gln Glu His Leu Glu Lys Thr Lys Pro His
                85   90   95

Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr Leu Asp Gly Met Ala
            100   105   110

Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe Glu Arg Asp Asp Ile
        115   120   125

Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly Ala Ile Met Met Ala
    130   135   140

Ile Gln His Thr Asp Phe Thr Ile His Gly Ser Asn Val Met Val Leu
145   150   155   160

Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg Thr Phe Ser Ala Leu
                165   170   175

Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser Ala His Leu Ala Arg
            180   185   190

Ile Met Glu Met Gly Leu Thr Pro Phe His Thr Asn Glu Leu Ala Glu
        195   200   205

His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr Ile Pro Ser Leu Ile
    210   215   220

Leu Asp Lys His Val Leu Ser Arg Met Thr Pro Arg Thr Leu Ile Leu
225   230   235   240

Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe Asp Phe Ala Glu Lys
245 250 255

Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu Pro Gly Ile Val Ala
260 265 270

Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val Leu Cys Asn Leu Leu
275 280 285

Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
290 295

<210> 94
<211> 1588
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1088)

<400> 94
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tcggcgctcg gcgcacgcgt aaaagtcgga gctcgcgact ccgcccacct cgccagaatc 180

atggagatgg gcctcactcc tttccacaca aacgaacttg cagagcatgt tgaaaatatc 240

gacatatgca tcaataccat tccaagcctg attctcgata aacatgtcct ctcacgaatg 300

acacccagaa cattaattct cgatttagca acccgtcccg gaggcacaga ttttgatttt 360

gccgaaaagc aaggcattaa agcgctgctt gctccaggac ttcccgggat cgtcgcgcct 420

aaaacggcgg gacagatcat tgccaatgtt ttgtgcaacc ttttgtctga attaacaact 480

gaccgaaagg ggctgtcata atg tcg atc aaa gga aaa aga atc gga ttt ggc 533
Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly
1 5 10

cta acg ggt tca cat tgt acg tat gat gcc gtt ttt ccg cag att gaa 581
Leu Thr Gly Ser His Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu
15 20 25

gcg ctg atc aac aaa ggg gct gaa gtc aga ccg gtc gtg acg cat act 629
Ala Leu Ile Asn Lys Gly Ala Glu Val Arg Pro Val Val Thr His Thr
30 35 40

gtc aag tcg acg gat aca cgc ttt gga gaa ggg gaa gaa tgg gtc aga 677
Val Lys Ser Thr Asp Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg
45 50 55

aga ata gaa gag ctg act gga ttt gaa gtc att gat tcc att ccg aaa 725
Arg Ile Glu Glu Leu Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys
60 65 70 75

gct gag cct ctc ggg ccg aaa aca ccg ctg gac tgc atg gtt gtt gcg 773
Ala Glu Pro Leu Gly Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala
80 85 90

cca ttg acg gga aat tcg atg agc aag ctt gca aac gcc cag acg gac 821

Pro Leu Thr Gly Asn Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp
95 100 105

agt ccg gtt ctc atg gcg gcc aaa gcg acg atg aga aac tcc cgt ccc 869
Ser Pro Val Leu Met Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro
110 115 120

gtc gtc ctc ggc att tca acg aat gac gcg ctc ggc ttg aac ggc gtc 917
Val Val Leu Gly Ile Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val
125 130 135

aac ttg atg agg ctg atg gcg gca aaa aat gtt tac ttt att ccg ttc 965
Asn Leu Met Arg Leu Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe
140 145 150 155

ggc cag gat gac cct tac aaa aag ccg aat tcg ctc gtc gcc aaa atg 1013
Gly Gln Asp Asp Pro Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met
160 165 170

gat ctt tta gtg ccg gcg gtc gaa gaa gcg ctc tcc cat aaa caa ata 1061
Asp Leu Leu Val Pro Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile
175 180 185

cag cct atc ctg gtc cat aat gat caa taaatctttt gaaaataaag 1108
Gln Pro Ile Leu Val His Asn Asp Gln
190 195

atgtaacaaa aaatatcaat caccacggca cacatctatg ttaaaataaa atgtaaaatg 1168

catagtcaac caatcgttta cgacgattaa ggtggaagga gttttacaat tgggcagagg 1228

attacatgta gcagtagttg gtgcgacagg cgctgtagga cagcaaatgt taaaaacact 1288

agaagacagg aattttgaac tggataaact gactttatta tcctcaaaac gttcagcagg 1348

tacgaaactg actttcaaag gcgaagagta cacagtagaa gaagctcgtc ctgagagctt 1408

tgaaggcgtc aacatcgcgc ttttcagcgc cgggggaagc gtttcgcagg cgcttgctca 1468

cgaggctgtc aaacgcgggg cgatcgtcat tgataatacg agcgcgttcc ggatggacca 1528

aaacactccg ctcgtcgtac ctgaggtcaa tgaggaagat ttgcacaagc acaacgggat 1588

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<211> 196
<212> PRT
<213> Bacillus licheniformis

<400> 95

Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly Leu Thr Gly Ser His
1 5 10 15

Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu Ala Leu Ile Asn Lys
20 25 30

Gly Ala Glu Val Arg Pro Val Val Thr His Thr Val Lys Ser Thr Asp
35 40 45

Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg Arg Ile Glu Glu Leu
50 55 60

Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys Ala Glu Pro Leu Gly

65 70 75 80

Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala Pro Leu Thr Gly Asn
85 90 95

Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp Ser Pro Val Leu Met
100 105 110

Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro Val Val Leu Gly Ile
115 120 125

Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val Asn Leu Met Arg Leu
130 135 140

Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe Gly Gln Asp Asp Pro
145 150 155 160

Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met Asp Leu Leu Val Pro
165 170 175

Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile Gln Pro Ile Leu Val
180 185 190

His Asn Asp Gln
195

<210> 96
<211> 2167
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1871)

<400> 96
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tatgatcggc tttttcttca caaatggacc ggtcatcaat tatgatacag cgaaacagtc 180

tgacctcgga ctgtttgccg aatattataa aggaatggcc gatgaaggcg tgtttctgcc 240

gccttcacag tttgaagggc tgttcttgtc aaccgctcat acggatgacg acattgagca 300

tacgattaaa gctgctgaac gcgtattcga aagaatcagc cgctccagat aaagaaaagg 360

gctgccggac attgccggcg gctctttttt gcatggtgcc gaaaacggct gctgattttt 420

ctgttcatat tctgcctgct tttcacatac atctttactg acatctaatt ttaaaaatta 480

ggtgaaggga ggatatcagt ttg ccg caa aac aat cgt ttg caa ttt tct gta 533
Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val
1 5 10

gaa gag tca atc tgt ttt caa aaa gga cag gaa gta tcc gaa tta tta 581
Glu Glu Ser Ile Cys Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu

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                15                          20                      25

tcg att tca ttg gat cct gac att acc gtt cag gaa gta aat gat tat      629
Ser Ile Ser Leu Asp Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr
        30                          35                      40

gta tcc ata cga ggg tca tta gag ctg aca ggc gaa tac aac ata gat      677
Val Ser Ile Arg Gly Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp
    45                      50                      55

caa acc cgg gag tat gca gag ctg cct gcg aca agc cga ttt gta gaa      725
Gln Thr Arg Glu Tyr Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu
60                  65                      70                  75

gat gta aag ctg aaa ggg gac ggc agc gca gag ctg acg cat tgt ttc      773
Asp Val Lys Leu Lys Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe
                80                      85                  90

cca gtg gat atc acc atc ccg aaa gac aaa gtc aat cat tta aac gac      821
Pro Val Asp Ile Thr Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp
            95                      100                     105

gta ttt gtt ttt att gac gct ttc gat tat cag ctg aca gat gcg agg      869
Val Phe Val Phe Ile Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg
        110                     115                     120

atg ctg acg att cag gct gat ttg gcg att gaa ggc ctc ttg aat gtg      917
Met Leu Thr Ile Gln Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val
    125                     130                     135

agc ggt gaa gcg ggt gaa gaa gaa ccg cgc act atg cct gcg gcc gtc      965
Ser Gly Glu Ala Gly Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val
140                 145                     150                 155

cat ccg gaa gag gag ctc gaa cct gcc tac aga tca cct tca aac gac     1013
His Pro Glu Glu Glu Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp
                160                     165                 170

gaa gat cag ggt gaa gag aaa gaa tat ttg atc cag ctt gac aga cct     1061
Glu Asp Gln Gly Glu Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro
            175                     180                     185

tac gaa gag cag gac gaa gaa cag gcg gaa gaa cat gat acc ggt gag     1109
Tyr Glu Glu Gln Asp Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu
        190                     195                     200

gaa acg gtt ccg att tac cag tcg ttt ctc gga aac gac aca gag gaa     1157
Glu Thr Val Pro Ile Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu
    205                     210                     215

gct aaa ccg ttt ttt aca gcg tct ttg tcg gcg gca gag cgt acg aag     1205
Ala Lys Pro Phe Phe Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys
220                 225                     230                 235

cgc gaa ata gaa aat caa aaa gaa gcc tct ctt gaa cag ccg gaa gaa     1253
Arg Glu Ile Glu Asn Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu
                240                     245                 250

gaa tat aag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat     1301
Glu Tyr Lys Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr
            255                     260                     265

gag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat gag ctg     1349
Glu Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu
        270                     275                     280

aaa aga gaa gaa gcg gaa gaa gag ccg gag ctg tcg cac agc tct tat     1397
Lys Arg Glu Glu Ala Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr
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                 285                  290                   295
caa cct cac gag gaa ctg aaa gag aac ccg ttc tac agt gtt cct cct      1445
Gln Pro His Glu Glu Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro
300                 305                 310                 315

ctt ctg aag gaa gac cag aat gac agg gag cct gag gct ttt gag gtt      1493
Leu Leu Lys Glu Asp Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val
                320                 325                 330

gag gtg aca cag gaa gca gaa gcg att gat gaa gaa gag gaa gcc ggg      1541
Glu Val Thr Gln Glu Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly
            335                 340                 345

cat acg att gaa atc ccg gaa tat tcg ttt cat gag cag acg gag ccc      1589
His Thr Ile Glu Ile Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro
        350                 355                 360

gaa gaa gaa aga gat gaa atg cag gca gcg gat gaa cag gaa gtg tca      1637
Glu Glu Glu Arg Asp Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser
    365                 370                 375

gca aag gaa aac gac aac gca ctc tat ttg aca aag ctg ttt aca aag      1685
Ala Lys Glu Asn Asp Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys
380                 385                 390                 395

cag gga gag gag gag ttt act cga atg agg atg tgc atc gtt cag caa      1733
Gln Gly Glu Glu Glu Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln
                400                 405                 410

aat gat acg att gat ctt ctg tgc gag cgc tat gat att aac gtc cag      1781
Asn Asp Thr Ile Asp Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln
            415                 420                 425

cag ctc atc cgg atg aat tcc ctt tcc ctt gac gag gaa tta aaa gag      1829
Gln Leu Ile Arg Met Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu
        430                 435                 440

gga cag atc ctt tat ata ccg gat tat caa aac agc cat gcc              1871
Gly Gln Ile Leu Tyr Ile Pro Asp Tyr Gln Asn Ser His Ala
    445                 450                 455

taatgcattg ataaaaatgt ggtgaagccg atggaaggca tccagtctgt tttaaatgag    1931
tacggtctta cgcctgaata tatggagtcc gtcagttcaa aggtgtggaa agtgtatacg    1991
gatcacggtg tatttgctct gaaaaaattg gcggcttcaa gaaacacccg cttcacggaa    2051
cagatgatca tgctggagga aaaaggctac aggcagttcg ttcctgtcta tcgaaaccgc    2111
acaggcgaat ttttaacgca agccggagaa gatgtctgct atctcatgcc ctggct        2167


<210>  97
<211>  457
<212>  PRT
<213>  Bacillus licheniformis

<400>  97

Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val Glu Glu Ser Ile Cys
1               5                   10                  15

Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu Ser Ile Ser Leu Asp
            20                  25                  30
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Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr Val Ser Ile Arg Gly
        35                  40                  45

Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp Gln Thr Arg Glu Tyr
    50                  55                  60

Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu Asp Val Lys Leu Lys
65                  70                  75                  80

Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe Pro Val Asp Ile Thr
                85                  90                  95

Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp Val Phe Val Phe Ile
            100                 105                 110

Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg Met Leu Thr Ile Gln
        115                 120                 125

Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val Ser Gly Glu Ala Gly
    130                 135                 140

Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val His Pro Glu Glu Glu
145                 150                 155                 160

Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp Glu Asp Gln Gly Glu
                165                 170                 175

Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro Tyr Glu Glu Gln Asp
            180                 185                 190

Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu Glu Thr Val Pro Ile
        195                 200                 205

Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu Ala Lys Pro Phe Phe
    210                 215                 220

Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys Arg Glu Ile Glu Asn
225                 230                 235                 240

Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu Glu Tyr Lys Leu Lys
                245                 250                 255

Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu
            260                 265                 270

Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu Glu Ala
        275                 280                 285

Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr Gln Pro His Glu Glu
    290                 295                 300
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Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro Leu Leu Lys Glu Asp
305 310 315 320

Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val Glu Val Thr Gln Glu
325 330 335

Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly His Thr Ile Glu Ile
340 345 350

Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro Glu Glu Glu Arg Asp
355 360 365

Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser Ala Lys Glu Asn Asp
370 375 380

Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys Gln Gly Glu Glu Glu
385 390 395 400

Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln Asn Asp Thr Ile Asp
405 410 415

Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln Gln Leu Ile Arg Met
420 425 430

Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu Gly Gln Ile Leu Tyr
435 440 445

Ile Pro Asp Tyr Gln Asn Ser His Ala
450 455

<210> 98
<211> 1955
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1463)

<400> 98
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tcaaagctta ttattacgaa agataactat attatgttca gtaacagaat catgaagaca 120
aaaaaggcga atttcatttc cttcaaatca aaaagacttt ggtgaagatc ccgctgtgaa 180
acaggggaga gccgagcagc gcctgcagca catcttcaga cagattggct ccattccccg 240
aaggacctca tcaatcacca ctttctcccg atttgccatg tcaacctgtt aagcatttac 300
caaacaggat gaaaaaattg gtttgtccgc acagcttacc tgaatacaat aaaaaataaa 360
gtatttctcg ggaaagcgca ggtttcaaca agacctgccc cgttcttgtc aaaaagcatt 420
ggattgtgca gtcatgtggg cgtctgtcac ggcataagcg cgccatgaat aggatataaa 480
gagagaatgg tgaggtgagt gtg ttg gaa agg gct gtt act tat aaa aac aac 533

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Val Leu Glu Arg Ala Val Thr Tyr Lys Asn Asn
1               5                   10

gga caa atc aat atc ata ttg aac ggt caa aag cag gtt ttg gcc aat        581
Gly Gln Ile Asn Ile Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn
            15                  20                  25

tca gag gct gaa gcc gaa tat cag gcc gca ctg caa aaa aat gaa gcc        629
Ser Glu Ala Glu Ala Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala
        30                  35                  40

aaa cac agc att ctg aaa gaa att gaa agg gaa atg aac acg ctg gtc        677
Lys His Ser Ile Leu Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val
    45                  50                  55

gga atg gag gaa atg aag cgc aat atc aag gaa atc tac gcc tgg att        725
Gly Met Glu Glu Met Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile
60                  65                  70                  75

ttc gtt aat aaa aag cgc gaa gaa caa ggc ctt aag gcc gga aaa cag        773
Phe Val Asn Lys Lys Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln
                80                  85                  90

gcg ctt cac atg atg ttc aaa gga aat ccg gga acc gga aaa acg acc        821
Ala Leu His Met Met Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr
            95                  100                 105

gtc gcc agg ctg atc ggc agg ctt ttt tac gaa atg aat gtt ctc tca        869
Val Ala Arg Leu Ile Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser
        110                 115                 120

aaa ggc cat ctg atc gag gcg gag cgc gcc gat ctc gtc ggt gag tac        917
Lys Gly His Leu Ile Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr
    125                 130                 135

atc ggc cat acg gcg caa aaa acg agg gat tta atc aaa aaa gcg atg        965
Ile Gly His Thr Ala Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met
140                 145                 150                 155

ggc gga atc ctg ttc atc gat gaa gcc tat tcc ctt gcc aga ggc gga       1013
Gly Gly Ile Leu Phe Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly
                160                 165                 170

gag aaa gac ttc ggc aag gag gca atc gat aca ttg gtc aaa cat atg       1061
Glu Lys Asp Phe Gly Lys Glu Ala Ile Asp Thr Leu Val Lys His Met
            175                 180                 185

gag gat aag cgc aac gaa ttc att tta atc ctc gcc gga tat tcg cgg       1109
Glu Asp Lys Arg Asn Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg
        190                 195                 200

gaa atg gat cat ttt ctt tca tta aac ccg ggc ctt cag tca agg ttt       1157
Glu Met Asp His Phe Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe
    205                 210                 215

ccg atc agc atc gat ttt ccc gat tac tca gtc agc cag ctg atg gac       1205
Pro Ile Ser Ile Asp Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp
220                 225                 230                 235

att gca aaa cgg atg atg gcg gaa agg gaa tat cag ttc agc cct gag       1253
Ile Ala Lys Arg Met Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu
                240                 245                 250

gct gaa tgg aag ctg aaa gac cat ctg atg gcc gtc aaa agt acg gtc       1301
Ala Glu Trp Lys Leu Lys Asp His Leu Met Ala Val Lys Ser Thr Val
            255                 260                 265

agc ccc gcg aag ttc agc aat ggc cgt ttc gtc cgc aac ctg atc gaa       1349
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Ser Pro Ala Lys Phe Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu
    270                 275                 280

aaa tcc atc cgg tcg cag gcg atg aga ctg ctg atg gga gac tgc tac      1397
Lys Ser Ile Arg Ser Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr
    285                 290                 295

tta aag aat gac ttg ata acc atc aaa agc cag gat ctc gac ttg aag      1445
Leu Lys Asn Asp Leu Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys
300                 305                 310                 315

gaa gac gcg ccg cac gta taatggcgcg ttcttttttt attttcgagg             1493
Glu Asp Ala Pro His Val
                320

atttctggca accgctccct tcgtttgtta tgatagtact gcttattgac taacgttaag    1553

aaaggaacat gatcacttga acgaacagga agtcatgaaa gagaaagcca tattagtcgg    1613

atgccagctt ccgcacgtgt ctgatgagcg tttttcatac tcgatggaag agctcgccgc    1673

gctgacgaaa acggccgacg gaacggttgt ttccacggtc acgcagaagc ggaaccgtgt    1733

ggatgctgct acatatatcg gaaaaggaaa agtagatgaa ttggcggtgc tctgtgaaga    1793

gctgtcgccc gatgttttaa tttttaatga tgaattgtcg ccgagtcagc tgaaagcgct    1853

tgtcacaacg cttgacgtga aaatcatcga ccggacgcag ttgatccttg atattttcgc    1913

caaacgcgcg aggacaaggg aaggaaagct gcaaattgag ct                       1955


<210>  99
<211>  321
<212>  PRT
<213>  Bacillus licheniformis

<400>  99

Val Leu Glu Arg Ala Val Thr Tyr Lys Asn Asn Gly Gln Ile Asn Ile
1               5                   10                  15

Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn Ser Glu Ala Glu Ala
            20                  25                  30

Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala Lys His Ser Ile Leu
        35                  40                  45

Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val Gly Met Glu Glu Met
    50                  55                  60

Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile Phe Val Asn Lys Lys
65                  70                  75                  80

Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln Ala Leu His Met Met
                85                  90                  95

Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr Val Ala Arg Leu Ile
            100                 105                 110

Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser Lys Gly His Leu Ile
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115 120 125

Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr Ile Gly His Thr Ala
130 135 140

Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met Gly Gly Ile Leu Phe
145 150 155 160

Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly Glu Lys Asp Phe Gly
165 170 175

Lys Glu Ala Ile Asp Thr Leu Val Lys His Met Glu Asp Lys Arg Asn
180 185 190

Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg Glu Met Asp His Phe
195 200 205

Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe Pro Ile Ser Ile Asp
210 215 220

Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp Ile Ala Lys Arg Met
225 230 235 240

Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu Ala Glu Trp Lys Leu
245 250 255

Lys Asp His Leu Met Ala Val Lys Ser Thr Val Ser Pro Ala Lys Phe
260 265 270

Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu Lys Ser Ile Arg Ser
275 280 285

Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr Leu Lys Asn Asp Leu
290 295 300

Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys Glu Asp Ala Pro His
305 310 315 320

Val

<210> 100
<211> 2082
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1607)

<400> 100
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aggcgggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat     180
tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaatg     240
tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg     300
aggaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa     360
ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt tttttatga      420
ataaaatcaa gccgtgccaa tttagcggca ggcatcataa cttattttgg aactttttga     480
atttagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt     533
                      Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe
                      1               5                   10

caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac       581
Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp
            15                  20                  25

agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga       629
Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg
        30                  35                  40

ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga       677
Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly
    45                  50                  55

acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg       725
Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly
60                  65                  70                  75

gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc       773
Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala
                80                  85                  90

gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa       821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu
            95                  100                 105

aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct       869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala
        110                 115                 120

act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg       917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met
    125                 130                 135

gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag       965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu
140                 145                 150                 155

gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag cgg cct gtc ggc      1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly
                160                 165                 170

agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg      1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu
            175                 180                 185

gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca      1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala
        190                 195                 200

gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac      1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr
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    205                 210                 215

ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc      1205
Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala
220                 225                 230                 235

gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa      1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln
                240                 245                 250

aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag      1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu
            255                 260                 265

cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat      1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His
        270                 275                 280

ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg      1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu
    285                 290                 295

aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat      1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His
300                 305                 310                 315

ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct      1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro
                320                 325                 330

ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct      1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro
            335                 340                 345

ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa      1589
Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys
        350                 355                 360

aaa gga gga ggg gaa aag tgacggttca ttttggttta atcggctgcg             1637
Lys Gly Gly Gly Glu Lys
    365

gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg    1697

ccgtcagtga tttgcaggaa gaaagaatga aggaagcgga agaatactat gcttccctcg    1757

ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta    1817

aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg    1877

cgctgctggc aggcaagcac gtcatcgtcg aaaaaccgat gaccttgtca ttacgggatg    1937

ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga    1997

tgcgccaccg gccgatcatg aaaaaactga aggaaacgat tgaggaagga aagctgggaa    2057

agatctactt gggcacggta tcgct                                          2082

<210>  101
<211>  369
<212>  PRT
<213>  Bacillus licheniformis

<400>  101

Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe Gln Thr Val Lys Gln
1               5                   10                  15
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Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile
20 25 30

Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
65 70 75 80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
260 265 270

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
275 280 285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
355 360 365

Lys

<210> 102
<211> 1975
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1472)

<400> 102
ctctcccgga ataaaaggaa cccgccacat ccttaaggcg gttgaatctt taaaagaaaa 60

atacgatttt cattttcacc tagtacaagg agtttctcat gaacaggcaa agaaaatcta 120

ccaaaaggct gatttgatca ttgatcagct tcatatcggc agctacggat tatttgccgt 180

cgaatcgatg gcaatgggga aacccgttat ctgctggatc agtgatttta tgaaggatca 240

ctatccttcc gaactgcctc ttataagagc aaatcccgcc aacattacag aggtgattga 300

aaatgtgctt aaaaaccggg atatgctgcc ggaaatcggc cagaaaggaa gaaagtatgc 360

agaagttcat catgatatgg tgaaaaacag caaaaaaaca ttggctgttt atcagtcgct 420

actttcggaa tgaagttgaa caactttccc gtcgcgggat ttgtatgtaa aaaaaaacga 480

aacaagcagg tgaacaattg atg agc gat atg aca gag tta tcc ggc cag cat 533
Met Ser Asp Met Thr Glu Leu Ser Gly Gln His
1 5 10

att ttc ata act ggc gga gca ggc ttt atc gga tcc tct tta ata gga 581
Ile Phe Ile Thr Gly Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly
15 20 25

aag ctg ata gag cgc aac agc gtc acc gta tat gac aat ttt tca aga 629
Lys Leu Ile Glu Arg Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg
30 35 40

gac tcc ctc cgg tat aag cct tac cgg gac cat cct cac ttg aaa gtg 677
Asp Ser Leu Arg Tyr Lys Pro Tyr Arg Asp His Pro His Leu Lys Val
45 50 55

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ctg cag gga gac att ttg gat ttg aac gcg ctt aaa aag gcg atc cag      725
Leu Gln Gly Asp Ile Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln
60                  65                  70                  75

ggg gcc agc cac att gtc cac gcc gcc ggc atc gct ggg att gac acg      773
Gly Ala Ser His Ile Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr
                80                  85                  90

gtc att caa aac ccg gtt aaa acg atg cag gtc aac atg atc ggt tca      821
Val Ile Gln Asn Pro Val Lys Thr Met Gln Val Asn Met Ile Gly Ser
            95                  100                 105

gcc aat ctg ctt gaa gcg gct gcc ggt tta acc gaa tgc aaa agg gtt      869
Ala Asn Leu Leu Glu Ala Ala Ala Gly Leu Thr Glu Cys Lys Arg Val
        110                 115                 120

gtc tgt ttc agt aca agc gaa gtg ttc ggc caa atc gct ttc aga gcg      917
Val Cys Phe Ser Thr Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala
    125                 130                 135

cgc gag acc agt cat act gtt tta gga gcg gtg gga gaa gcc cgc tgg      965
Arg Glu Thr Ser His Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp
140                 145                 150                 155

aca tat gct gtc agc aaa ctc gcc gag gag cat atg gca tat gcc tat      1013
Thr Tyr Ala Val Ser Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr
                160                 165                 170

ttt aaa gaa ctt ggg ctt ccg acc gtc acc gtc cgc cct ttt aat gtt      1061
Phe Lys Glu Leu Gly Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val
            175                 180                 185

tat gga ccg gaa caa gtc ggc gaa ggc gcc atc aaa acg atg gtt cac      1109
Tyr Gly Pro Glu Gln Val Gly Glu Gly Ala Ile Lys Thr Met Val His
        190                 195                 200

aga gct ctg tta gat gag ccg atc tat att cac ggc gat gga acg caa      1157
Arg Ala Leu Leu Asp Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln
    205                 210                 215

atc cgg gcc tgg tgt tac gta gat gac atg atc gac gga att ttg cgt      1205
Ile Arg Ala Trp Cys Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg
220                 225                 230                 235

tgt ttg acg atg aag gaa gcc atc gga gag tct ttc aac atc ggc aat      1253
Cys Leu Thr Met Lys Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn
                240                 245                 250

gaa cgc act gtg atc acc gta tac gga ttg gca agc acg att atc aga      1301
Glu Arg Thr Val Ile Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg
            255                 260                 265

gtt ctc gga tca aaa tca caa atc ttc ttt ggg gag aaa aaa gaa gcc      1349
Val Leu Gly Ser Lys Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala
        270                 275                 280

gat att gaa ctg cgc atc cct cag gtc aat aaa gca aaa gag atg ctc      1397
Asp Ile Glu Leu Arg Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu
    285                 290                 295

ggt ttc agc gct aaa gtt gat ctg gaa gaa ggc atc aga aga aca gct      1445
Gly Phe Ser Ala Lys Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala
300                 305                 310                 315

gaa agc att aaa aaa aat ttg gat caa taagaaagga ggcgctattg            1492
Glu Ser Ile Lys Lys Asn Leu Asp Gln
                320
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ttgaaacaat ggaaaagcga aggaaaaggt gaattcactc tttcccagct tgggggctgt 1552

ggcgaaaatg tcgttatcga agacggggtc cgcatttttc atccggaaaa catctatatc 1612

ggagataacg tttatatcgg ccatgacacg attttaaaag gctattataa gcatgacctg 1672

atcatcggtt caaacagctg gatcgggcag caatgtttta tacacggtgc cggcggggtt 1732

acaatcggag aatttgcagg aattggtccg aacgtccgga tacatgccgc ttaccatacc 1792

gatcctgata aacccgacag taccattttg ttttcgccgc ttacattcgc tcctattcat 1852

attgaagaaa actgcaacat cgggatcggt gcgtctatcc tagcaggcgt tacgataggc 1912

gcccactcca aaatcggagc aaatgccgtc gtcaatcgca atattccccc gtacagcata 1972

gca 1975

<210> 103
<211> 324
<212> PRT
<213> Bacillus licheniformis

<400> 103

Met Ser Asp Met Thr Glu Leu Ser Gly Gln His Ile Phe Ile Thr Gly
1 5 10 15

Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly Lys Leu Ile Glu Arg
20 25 30

Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg Asp Ser Leu Arg Tyr
35 40 45

Lys Pro Tyr Arg Asp His Pro His Leu Lys Val Leu Gln Gly Asp Ile
50 55 60

Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln Gly Ala Ser His Ile
65 70 75 80

Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr Val Ile Gln Asn Pro
85 90 95

Val Lys Thr Met Gln Val Asn Met Ile Gly Ser Ala Asn Leu Leu Glu
100 105 110

Ala Ala Ala Gly Leu Thr Glu Cys Lys Arg Val Val Cys Phe Ser Thr
115 120 125

Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala Arg Glu Thr Ser His
130 135 140

Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp Thr Tyr Ala Val Ser
145 150 155 160

Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr Phe Lys Glu Leu Gly

165 170 175

Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val Tyr Gly Pro Glu Gln
180 185 190

Val Gly Glu Gly Ala Ile Lys Thr Met Val His Arg Ala Leu Leu Asp
195 200 205

Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln Ile Arg Ala Trp Cys
210 215 220

Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg Cys Leu Thr Met Lys
225 230 235 240

Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn Glu Arg Thr Val Ile
245 250 255

Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg Val Leu Gly Ser Lys
260 265 270

Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala Asp Ile Glu Leu Arg
275 280 285

Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu Gly Phe Ser Ala Lys
290 295 300

Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala Glu Ser Ile Lys Lys
305 310 315 320

Asn Leu Asp Gln

<210> 104
<211> 1213
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(710)

<400> 104
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tggcaagcca gacgcttgaa agcatgtatg ccatcaacgc ggtcacgagc acgccggttt 120
tgcgcccttt aatcggcatg gataagacgg aaatcatcga aaaagcgaag gaaatcgata 180
cgtacgatat cagcatacgt ccgtacgaag actgctgcac gatctttacg ccttctgcgc 240
cgaaaacgcg tccgaaaaaa gagaaaatcg aacactttga aagctacaca gatttcgaac 300
cgcttatcaa cgaagctgtg gaaaacacgg aaacgattgt tttgagcagc aaagcggaaa 360
cgaaagatca atttgcggat tttttctaaa ggaatattca atcaaacatc tttgtctgtt 420

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tttgcataca attaccaaac attctttgta tgaagtcatg tgtttttaca caatctatac      480

tcacaaggag gtgagaacac atg gct caa aac aac aga caa agc agt tct aac      533
                      Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn
                      1               5                   10

caa cta ttg gtt cct ggt gct gct caa gct atc gac caa atg aaa ttc        581
Gln Leu Leu Val Pro Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe
            15                  20                  25

gaa atc gct tct gaa ttt ggc gtt aac ctt gga gca gaa act act tct        629
Glu Ile Ala Ser Glu Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser
        30                  35                  40

cgt gca aac ggt tca gtt gga gga gaa atc act aag cgt tta gtt tct        677
Arg Ala Asn Gly Ser Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser
    45                  50                  55

ttc gct caa cag caa atg ggt gga aca caa caa taattaaaat taaaaagcaa      730
Phe Ala Gln Gln Gln Met Gly Gly Thr Gln Gln
60                  65                  70

tggataatgg gtggggttta atccccactc ttttttatgt tctgcaaaat aggcatttcg      790

gaatacaatt gtatgaaagg attatgtata ataaaaagat ggcacaagac aaggagatgg      850

aagggttgag aagagaagat ttgattgcgc cggagaagta taatgcggtt gatgaaattg      910

aaaaatttaa atcttcccgc gataagaccg cattgatctg ggaagatgaa tcagggcgtc      970

aagtgtcatg gtcctatgaa aaattgattg aaaaggctta caaaatcggc agcatattga     1030

cccgttctgg actgaaaaaa ggtgacaagc ttatcgtgat gatgccgcgg ataccggaaa     1090

cgtatgccgt gtacatggcc attttaaaag ctggaatggt ggtcatccca tgttccgaaa     1150

tgcttcgggc gaaagacttg gattacagga tcaagcatgc aggcgtcaaa ggagccgtcg     1210

tat                                                                   1213


<210>  105
<211>  70
<212>  PRT
<213>  Bacillus licheniformis

<400>  105

Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn Gln Leu Leu Val Pro
1               5                   10                  15

Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe Glu Ile Ala Ser Glu
            20                  25                  30

Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser Arg Ala Asn Gly Ser
        35                  40                  45

Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser Phe Ala Gln Gln Gln
    50                  55                  60

Met Gly Gly Thr Gln Gln
65                  70
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<210> 106
<211> 1196
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(695)

<400> 106
cattgtacga gacttaaaat cggtttatga cttcgaaacg atccgtccga tcttaacaac 60

gatttttaat acgattacag accgctccga tgatgtagtg agtccgctgc gcttttatga 120

agggtatgcg cgggtccttg atcatgtgta ccagatcaaa gactatacgc tcaataaatc 180

ggcgcttgaa aaaatcgtca ttgagcagac tggacagctc cgcgattttt ataaagatct 240

ggccgatccc gaatggaaca aagcgagaga catcaccgca gtcactgtgc tgtccgtcat 300

cgcttcgcac attcaggcga ccgcacattc catgattgac agcgtcttct taaaatatga 360

aatgaaataa tcgccgaccg gcgcgcctgg cttgccaatt gccaggcgtt tttttgccct 420

tcaacaattg ccagcataaa aagcctcagt ccaaatcaaa ctaaacaagc agtaccaatt 480

gaaaaaggag ttgagaatgc atg gca aga acg aat aag ctc ctc gtt ccc ggg 533
Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly
1 5 10

gca gag cag gtt tta gac cag ttc aaa tac gaa atc gcc caa gag ttc 581
Ala Glu Gln Val Leu Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe
15 20 25

ggc gtc cag ctc ggc tcg gac tcg gtc gct cgc tca aac gga tct gta 629
Gly Val Gln Leu Gly Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val
30 35 40

ggc ggg gaa atg aca aaa cga ctt gta cag cag gca caa gct caa ttg 677
Gly Gly Glu Met Thr Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu
45 50 55

aat ggg cat aat gac aaa taaataccct atggattatt cgccgggccc 725
Asn Gly His Asn Asp Lys
60 65

gctcggcgga tattcttgtt tattcgtttg gtcagaaggc tttttctcct tttggtaagg 785

aagtgattta gagctctctt gatttgaacc ggaaccgctt tttggcgttc cttcctccgt 845

ctgctgaccg tctttgtcat tatggttatg ttcctgaggg tttttggtat taggggaatt 905

tgactccttt tctttttcca tttcttgatc aggttgagac tgatcttcat ctgaaggttt 965

ttcgccgtcc ggatgatctt ccgtatctgc ttctttatca tccgtatgct gttccggctg 1025

atcttcttct ttcacagctt tctccttttc tcctgtgttt tcttcctgat tttgatcatc 1085

ttttttattt tcattgtcat catctttgtt tttgtcttct aattcatctt tgtgggaacg 1145

gatataacgg cctgttgaga tgccttcttt ttgggctttt gcacgcgtat c 1196

<210> 107
<211> 65
<212> PRT
<213> Bacillus licheniformis

<400> 107

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Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly Ala Glu Gln Val Leu
1               5                   10                  15

Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe Gly Val Gln Leu Gly
            20                  25                  30

Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val Gly Gly Glu Met Thr
        35                  40                  45

Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu Asn Gly His Asn Asp
    50                  55                  60

Lys
65
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<210> 108
<211> 2279
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1463)

<400> 108

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acacgcagcc aaaatgaaat ggcctatcat atacattaat gaccattttg gaatttggca      60

agcggatatt gctgccatta tcaagaaatg caaaaacggc aggagcgaat atatcatcga     120

ccggcttgca ccgaatgaca gcgattattt tttaatcaaa ccaaagcact cagcctttta     180

cggcactgct cttgaaacat tgctgcatga acttcatgtc gatcatttga tcatcactgg     240

gatcgcaggc aatatctgcg tattatttac ggcaaacgat gcttatatgc gggagtacga     300

gattacgatt ccgcgcgatt gcatcgcctc aaacaatgaa aaagacaaca aatacgcctt     360

gacgatgatg gaaaatgttc tgttcgccaa tatcacgacg gctaaggcga ttacctccga     420

aacttagagc atgaaacact tcctttcatc atatagtggt agcaatgaga aaggaggcgt     480

ttcccattca gatttatgtc gtg aaa aga ggc gat acc ctt tac caa atc gcg     533
                      Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala
                      1               5                   10

aat cgt tac cga aca aca gtt aat gaa att gtc gcg acg aat gaa att       581
Asn Arg Tyr Arg Thr Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile
            15                  20                  25

ccg aac ccg aat cgg ctt gtt gtc gga caa acc atc gtg atc ccg atc       629
Pro Asn Pro Asn Arg Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile
        30                  35                  40

gcc ggc gag ttt tat gag gtc aga cag gga gat aca tta gca tca atc       677
Ala Gly Glu Phe Tyr Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile
    45                  50                  55

gga gca cgc ttt aat att tct ccg gct gaa ctg gcg agg atc aac cgc       725
Gly Ala Arg Phe Asn Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg
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60 65 70 75

att cag gtt agc gcc gtt tta ccg gtc gga ctg ctg ctt tac atc ccc 773
Ile Gln Val Ser Ala Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro
80 85 90

cct cgg cca aga cgg aac att gaa aca aac gcc tat atc gaa cct cgg 821
Pro Arg Pro Arg Arg Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg
95 100 105

gga gaa agc gta agc ccc gct ttg cag cag gcg gca aga gag gct tcg 869
Gly Glu Ser Val Ser Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser
110 115 120

cca tac ttg acc tat ctg ggc gct ttc agc ttc cag gcg aag cgg gac 917
Pro Tyr Leu Thr Tyr Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp
125 130 135

ggc aca ctc gaa gaa ccg ccg ctg aac aac tta aaa gaa att gcc gac 965
Gly Thr Leu Glu Glu Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp
140 145 150 155

aga cat cgg act acg atg atg atg att gtc acc aat ctc gaa aat gaa 1013
Arg His Arg Thr Thr Met Met Met Ile Val Thr Asn Leu Glu Asn Glu
160 165 170

gct ttc agc gac gaa ctc ggc agg atc att ctg acg gac cag aat gta 1061
Ala Phe Ser Asp Glu Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val
175 180 185

aaa aac aga ttg ctc gat aac atc gtt gca gcg gcc aga aga tac ggt 1109
Lys Asn Arg Leu Leu Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly
190 195 200

ttt aaa gac atc cat ttt gac ttc gaa tac tta agg ccc gaa gat aga 1157
Phe Lys Asp Ile His Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg
205 210 215

gaa gcc tat aat cag ttt tta cgg gat gcc cgg gcc cgc ttc agg cag 1205
Glu Ala Tyr Asn Gln Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln
220 225 230 235

gaa ggc tgg ctc atc tca acc gcg ctt gct ccg aaa acg aga gcg gat 1253
Glu Gly Trp Leu Ile Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp
240 245 250

cag ccc gga caa tgg tat gaa gcc cat gat tac cgg gcc cac ggc gaa 1301
Gln Pro Gly Gln Trp Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu
255 260 265

att gtc gat ttc gtc gtg ctg atg aca tat gag tgg ggc tac agc gga 1349
Ile Val Asp Phe Val Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly
270 275 280

ggg ccc ccg atg gcg gta tcg ccg atc ggg ccc gtc cgg gac gtg atc 1397
Gly Pro Pro Met Ala Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile
285 290 295

gaa tac gca ctc acg gaa atg ccc gcc agc aaa atc gtc atg gga cag 1445
Glu Tyr Ala Leu Thr Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln
300 305 310 315

aaa ctg tac ggc tat gac tgacgctccc ctatatgcac agcgggaccc 1493
Lys Leu Tyr Gly Tyr Asp
320

gttggccaag accaatccgg ccccaacggg gggattgaga tcgcgagcga gaacaatgcg 1553

gcgatacagt acgatgaaac agctcaggct ccaaacttcc gctatacgga caatgccggc 1613

aaacagcatg aagtatggtt tgaagacgcc cgctcgattc aggcaaagtt tgatctgatt 1673

agggaattga atttaagggg aatcagctat tggaagctcg gcctgtcctt cccgcaaaac 1733

tggctcttga tagccgatca atttaatgtt gttaaagaga cgttcccaag ttaaaggaac 1793

gtttttttc atggcagcgg atgatgatgt gatacaatat gtatggttca caaatgaatt 1853

tctttagtag gaggacacct atgaatacag cccctttcat tgctgtcgaa ggccccatcg 1913

gcgcgggaaa aacaaccttg gccagcatgc tctccgaaaa gctctcactc tctttggtca 1973

aagaaatcgt cgaagaaaac ccttttcttg ataaatttta tgatgaaaaa gatgaatgga 2033

gctttcagct tgagatgttt ttcctctgca atcgctataa gcagcttgaa gataccgaga 2093

aaaagtattt gcatcatcac atgcccgttg tttcggacta tcatatttat aaaaacctca 2153

tttttgccga acggacgctg gaaggcaaaa aacttgagaa atacagaaaa atttatcagc 2213

tgcttacaga agatctgccg aaaccaaacg tcatcattta cataagagcg agtcttccaa 2273

ctttat 2279

<210> 109
<211> 321
<212> PRT
<213> Bacillus licheniformis

<400> 109

Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala Asn Arg Tyr Arg Thr
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Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile Pro Asn Pro Asn Arg
20 25 30

Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile Ala Gly Glu Phe Tyr
35 40 45

Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile Gly Ala Arg Phe Asn
50 55 60

Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg Ile Gln Val Ser Ala
65 70 75 80

Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro Pro Arg Pro Arg Arg
85 90 95

Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg Gly Glu Ser Val Ser
100 105 110

Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser Pro Tyr Leu Thr Tyr
115 120 125

Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp Gly Thr Leu Glu Glu
130 135 140

Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp Arg His Arg Thr Thr
145 150 155 160

Met Met Met Ile Val Thr Asn Leu Glu Asn Glu Ala Phe Ser Asp Glu
165 170 175

Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val Lys Asn Arg Leu Leu
180 185 190

Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly Phe Lys Asp Ile His
195 200 205

Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg Glu Ala Tyr Asn Gln
210 215 220

Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln Glu Gly Trp Leu Ile
225 230 235 240

Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp Gln Pro Gly Gln Trp
245 250 255

Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu Ile Val Asp Phe Val
260 265 270

Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly Gly Pro Pro Met Ala
275 280 285

Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile Glu Tyr Ala Leu Thr
290 295 300

Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln Lys Leu Tyr Gly Tyr
305 310 315 320

Asp

<210> 110
<211> 2011
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (252)..(1508)

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ccttcccaag cccctatcac ctcctttatt tgaaggatac actttctaga ctgttcagtc 120

aagaattatc cgcttcacgg ttctattcac cattccagct gtaaaaaacg gcgcatgatc 180

cttctgcaac ggtcatagac atagcataaa accccctgtc acatacagag gaacaaaagg 240

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aagtgtgcca g ttg ttt att tat aca gtc cag ccg gga gat tca cta ttt      290
             Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe
             1               5                   10

gtc atc ggc gcc aag ttc gga att tcg att gac cag atc cga ttg gcg      338
Val Ile Gly Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala
    15                  20                  25

aat ggg ttg atc gca aca aac att gtc ccc gga cag gct ctt tta ata      386
Asn Gly Leu Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile
30                  35                  40                  45

ccg ctt tat aca tat acc gtt cag ccg gga gac agt tat tac acg att      434
Pro Leu Tyr Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile
                50                  55                  60

gcc cgc cgg acg ttt gta tcc gtc gaa gca ttg caa aaa gca aat ccg      482
Ala Arg Arg Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro
            65                  70                  75

tct gta acc cct tcc aat atg agg ccg ggg ata aaa gtg atg att ccg      530
Ser Val Thr Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro
        80                  85                  90

gaa ttg ccg aaa aaa ccg atc act gct tta gga tat tac aca ctg aga      578
Glu Leu Pro Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg
    95                  100                 105

aac ccc cgg tta gac cag gaa ttg att cat aat ttt gcc cca tac gcc      626
Asn Pro Arg Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala
110                 115                 120                 125

acg tat ctg gca ttt ttt gaa tac cac att tca agc gac gga tcg tta      674
Thr Tyr Leu Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu
                130                 135                 140

agc gag ctg aat gat tca ccg gcc gta caa acg gct tgg aga cgg cgc      722
Ser Glu Leu Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg
            145                 150                 155

gtt cct ccc ctc atg aca gtc acc aat cta act gaa tca ggc ttc agt      770
Val Pro Pro Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser
        160                 165                 170

ccg tct ctt gcg cac cgc gta tta aat cag cct gcc gta aga aat cgc      818
Pro Ser Leu Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg
    175                 180                 185

ctc atc gac aat att gtc caa acg att tcc aga aaa gga tat gca ggc      866
Leu Ile Asp Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly
190                 195                 200                 205

gtc aat att gat ttc gaa cag att ttg gag gaa gac aga gat tta ttt      914
Val Asn Ile Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe
                210                 215                 220

tca ggt ttt ctc cgc ctg ttg aaa gag cgg ctg aag ccg tcc ggc tat      962
Ser Gly Phe Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr
            225                 230                 235

gtg ttg acg att gcc gtt ccg ccg aaa aca aat gaa aat atc gcc tgg     1010
Val Leu Thr Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp
        240                 245                 250

ctg aaa ggg tat gac tat ggc gga atc ggt gca gtg agc gac ctt atc     1058
Leu Lys Gly Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile
    255                 260                 265
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ttc atc atg gca tac gac tgg cac cac ggg aca agc gag ccc ggc ccc      1106
Phe Ile Met Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro
270                 275                 280                 285

att gct ccg atc aat gaa gtc cgg caa aca att caa ttt gct ctc cgc      1154
Ile Ala Pro Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg
                290                 295                 300

cat gtc ccc aaa gaa aaa atc gtt ctc ggc ttt ccg ctt tac ggc tat      1202
His Val Pro Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr
            305                 310                 315

aac tgg acc ctg ccc tat cag ccc ggt gcc gta tac ccc gga atc gcc      1250
Asn Trp Thr Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala
        320                 325                 330

aac caa gac gcc gtt cag ctc gcc atg aag cac cag gca ccg att caa      1298
Asn Gln Asp Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln
    335                 340                 345

tat gat aca aat tct gag tcc cct ttt ttc aga tac acc gat gaa cag      1346
Tyr Asp Thr Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln
350                 355                 360                 365

ggc aga cgg cat gtc gta tgg ttt gaa gac gca cgc agc atc gga aaa      1394
Gly Arg Arg His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys
                370                 375                 380

aaa ctg cag ctg atc acc gaa tac gga ctt gac ggc ggc ggc gtc tgg      1442
Lys Leu Gln Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp
            385                 390                 395

cag ctc aca ctc agt ttt ccg caa gga aca tgg ctc ttg acc aaa ttc      1490
Gln Leu Thr Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe
        400                 405                 410

ttt cgc gtc cga aaa gtc tgacatcatt atgtgattta ttgtaaaata              1538
Phe Arg Val Arg Lys Val
    415

acaaaccgaa taatcccgct aacgaatttt gatactaaag atgtgtcctt cacacaataa    1598

caaatttgaa aggaatgttt gcgattgaat aatgcgatcc atgaaacatt ggagctgcat    1658

gagctgttaa tgtttaaaaa cctttgtctg acaaagtcat caacaatgac gggaatggtt    1718

caggatcaag agcttcgcga catcttggag cgtgatgcat cccaaacaaa gcatcagatc    1778

gagcatttac aaggtctatt gtcagtgaga ggtgaaaccg tatgaacgaa ttcatccaaa    1838

acatgacagg catgggcgcg atgactgaac aagtcattgc caccgatttt ttaatctcgg    1898

caaaaaccgg tgtcaaaaac attgccacag ctatcacgga aacatcttct ccagaagtgc    1958

gcgaaacgct taagcagtat ttaaacgacg cgattgacac ccatgaacag atc           2011


<210>  111
<211>  419
<212>  PRT
<213>  Bacillus licheniformis

<400>  111

Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe Val Ile Gly
1               5                   10                  15
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Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala Asn Gly Leu
20 25 30

Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile Pro Leu Tyr
35 40 45

Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile Ala Arg Arg
50 55 60

Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro Ser Val Thr
65 70 75 80

Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro Glu Leu Pro
85 90 95

Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg Asn Pro Arg
100 105 110

Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala Thr Tyr Leu
115 120 125

Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu Ser Glu Leu
130 135 140

Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg Val Pro Pro
145 150 155 160

Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser Pro Ser Leu
165 170 175

Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg Leu Ile Asp
180 185 190

Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly Val Asn Ile
195 200 205

Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe Ser Gly Phe
210 215 220

Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr Val Leu Thr
225 230 235 240

Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp Leu Lys Gly
245 250 255

Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile Phe Ile Met
260 265 270

Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro Ile Ala Pro
275 280 285

Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg His Val Pro
    290   295   300

Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr Asn Trp Thr
305   310   315   320

Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala Asn Gln Asp
                325   330   335

Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln Tyr Asp Thr
            340   345   350

Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln Gly Arg Arg
        355   360   365

His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys Lys Leu Gln
    370   375   380

Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp Gln Leu Thr
385   390   395   400

Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe Phe Arg Val
                405   410   415

Arg Lys Val

<210> 112
<211> 2014
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (558)..(1511)

<400> 112
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gccggggtca actgccgttt taaagccgat atggtctcct gccggacaag cggggtgtca 120

catggccgaa aaaatatagc attccccttc cgcccgctcc atggctgtgt acataccggc 180

aagcggccct ttccctctgt acgggtcgat atcttccagc accgcttttt tcccgagttc 240

tataaaccgc tccgtcaagc ccggacggct caatatcagg acgtcgtctc ccagcgcctg 300

tttgcaccat tgataaagcg gcttgccttt ccagcgggca aacgccttcg gttccccaaa 360

acggcgcgaa agccccccctg ataatatgac atgtatttct ttcatacggc tcaaccttcc 420

ttcgcgtgtt cctgcctgcg aacatcatag caaaacttta gaaatccgaa caagtctgta 480

aaatctcttt ttcaaaaggc atggcgggtt tcatttatgc atattgtagt tgtaacattt 540

atagggggct ggtcacc atg aaa aaa aca tcg ggt tcg ctg cct tat ttt 590
                   Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe

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                    1               5                   10

caa gat tta tca cag gaa aac ctt ttt tta aaa gct gag ctg gca aga        638
Gln Asp Leu Ser Gln Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg
            15                  20                  25

tca cat caa ttg ata cac gag ctt gaa gca agc tat ttt cac cag aaa        686
Ser His Gln Leu Ile His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys
        30                  35                  40

aat cat aag ctc agc cgg gaa aac gca gca atg aaa cag cag ctt cag        734
Asn His Lys Leu Ser Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln
    45                  50                  55

cag ctg tca ttc gaa ctg gag cgg att tcg gca aac aag gaa gac aag        782
Gln Leu Ser Phe Glu Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys
60                  65                  70                  75

tcg gcc gaa acg ctc aac cgg ata aaa agc gaa ttg ctg agt aaa atc        830
Ser Ala Glu Thr Leu Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile
                80                  85                  90

gtc gtt ctt cag gag ctt ctt caa aaa gaa acc tat gca aga aaa caa        878
Val Val Leu Gln Glu Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln
            95                  100                 105

gag ata gaa gaa aag cac cgc ctt cat tta aca aat gta aaa gcc gaa        926
Glu Ile Glu Glu Lys His Arg Leu His Leu Thr Asn Val Lys Ala Glu
        110                 115                 120

gaa gag aaa aaa agc tta cat agc caa ata gaa tac gaa aag ctt cat        974
Glu Glu Lys Lys Ser Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His
    125                 130                 135

gca gaa aga gaa aaa acg ctg agg gaa aaa aag gaa cag gag ctc aaa       1022
Ala Glu Arg Glu Lys Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys
140                 145                 150                 155

aac gct gca tac gaa aat gcc cgc ctg aaa gat gaa ctt cat gct aaa       1070
Asn Ala Ala Tyr Glu Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys
                160                 165                 170

agt ctt cag ctc aaa caa atc gaa act gat gtt gcg gta tta aaa gag       1118
Ser Leu Gln Leu Lys Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu
            175                 180                 185

cgg gtg acg gaa acg aaa agc cgg ctt ttg gag gct gaa aaa aca aaa       1166
Arg Val Thr Glu Thr Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys
        190                 195                 200

gaa gcg ctg ttt tat gaa acg att ctc tct tat aaa agg caa ctc gat       1214
Glu Ala Leu Phe Tyr Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp
    205                 210                 215

gaa agt gat aag tgg atc gct tct cat ttt gcc gat att gat gca ttt       1262
Glu Ser Asp Lys Trp Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe
220                 225                 230                 235

cag cag acg gag aag gcg ctt gaa caa aac gag gag gtt ttt gaa cgg       1310
Gln Gln Thr Glu Lys Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg
                240                 245                 250

aca gaa cag atc gag gcg gtg ctt caa act gtt aca gag caa gtt gat       1358
Thr Glu Gln Ile Glu Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp
            255                 260                 265

cag ctc caa caa caa ttg agc gcc att caa caa aat tat acg aaa atg       1406
Gln Leu Gln Gln Gln Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met
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270 275 280

gat caa aaa ata aca gaa tgg aaa aaa cag gcg aaa gaa gaa aca ccc 1454
Asp Gln Lys Ile Thr Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro
285 290 295

ccg caa aaa tgg gtc tat caa att aaa cgc aaa gac aaa gaa aca aaa 1502
Pro Gln Lys Trp Val Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys
300 305 310 315

cct tta aat taaataccac tttaaggaat aatttggttt ttacaaaaaa 1551
Pro Leu Asn

accgcttgag tagattgtct caagcagttg attgggcggc ggcgtataaa gcggccgcct 1611

ttatgttccc ttaaaatgga aacgctatct gaaaaagcaa gggtttgacc tattgctgct 1671

ctgtctcagt agaaatctca ccctctaata tatattgacc gcggtatggt tttttgactt 1731

ccgggtacat tttaatcagg ctttgcataa aggttgtcat attagggatc tcaagtccgc 1791

tctctttttc gatttctttt tgaagttcgg agcttttgat ggccgcatta tggcgtttta 1851

atgttttaat cgccgcttca cgcaattttg cagcttttga gcctggacgt gctgtacccc 1911

ttctgcgcct tgtcgttcca tctggaattc cggcaggcag tgaggaggtt tgcggagaag 1971

tctgctgctg gttcttttga gatgcttgcg gctgctgttg ctg 2014

<210> 113
<211> 318
<212> PRT
<213> Bacillus licheniformis

<400> 113

Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe Gln Asp Leu Ser Gln
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Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg Ser His Gln Leu Ile
20 25 30

His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys Asn His Lys Leu Ser
35 40 45

Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln Gln Leu Ser Phe Glu
50 55 60

Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys Ser Ala Glu Thr Leu
65 70 75 80

Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile Val Val Leu Gln Glu
85 90 95

Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln Glu Ile Glu Glu Lys
100 105 110

His Arg Leu His Leu Thr Asn Val Lys Ala Glu Glu Glu Lys Lys Ser
115 120 125

Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His Ala Glu Arg Glu Lys
    130   135   140

Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys Asn Ala Ala Tyr Glu
145   150   155   160

Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys Ser Leu Gln Leu Lys
                165   170   175

Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu Arg Val Thr Glu Thr
            180   185   190

Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys Glu Ala Leu Phe Tyr
        195   200   205

Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp Glu Ser Asp Lys Trp
    210   215   220

Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe Gln Gln Thr Glu Lys
225   230   235   240

Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg Thr Glu Gln Ile Glu
                245   250   255

Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp Gln Leu Gln Gln Gln
            260   265   270

Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met Asp Gln Lys Ile Thr
        275   280   285

Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro Pro Gln Lys Trp Val
    290   295   300

Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys Pro Leu Asn
305   310   315

<210> 114
<211> 2341
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1838)

<400> 114
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agcccgttct aaacggcagc atcgagaaaa aagcagaccg cgaatcagtg gaagctgtgg 180

aagaagcggt agatcaaaat aaaaaagaaa cagaagcttt atttttctat aatcccgaca 240

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tcgcttctga tgactggatt aaaacgagaa aagtcgtgaa gcgcatcggc aatcatgtct      300
ttgcgatcta gaaagcagtc agggccattc gccttggctg cttttttgt gcgattcttt       360
cttacgcatt atcatctttc acagcccaag aaaaaattta tttttgatac tttatgaaaa      420
tcaattttca attaaaaaga aaataatttt tagacttgtc tcatatgatg ggataaaccc      480
gtgagacaag gagagacctc atg aac cgt ttt gta aaa gga atc gtt ctt ctt     533
                      Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu
                      1               5                   10

tcg cta gct gct ttt ttt gca gaa tgt ctt gaa ttc gtc atc aac atg       581
Ser Leu Ala Ala Phe Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met
            15                  20                  25

att ctt gca cgg gag ctt ggc gag cat ggc atg ggg ctc tac atg agt       629
Ile Leu Ala Arg Glu Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser
        30                  35                  40

gtt ttg cct tcc att ttt ttg gtc gtg gtg att gcg agc ctt gag ctg       677
Val Leu Pro Ser Ile Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu
    45                  50                  55

ccc gta tca ata tcg aag ttt atc gcc gag tcc aac ccg aag ctg cac       725
Pro Val Ser Ile Ser Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His
60                  65                  70                  75

gaa agc atg ctg aaa cat gca ttg cgg atg act gcg gtc tgc acg gtt       773
Glu Ser Met Leu Lys His Ala Leu Arg Met Thr Ala Val Cys Thr Val
                80                  85                  90

ttc tcc acg gca gcc gca gtg atc att ctt cca ttt att ccg gtt ttt       821
Phe Ser Thr Ala Ala Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe
            95                  100                 105

gat tct tac cac cct cta atc aga gga ctt gtg atc ggg atg att cct       869
Asp Ser Tyr His Pro Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro
        110                 115                 120

acg gtt gca ttc aca tcg atc gcg aga ggc tac ttc atg ggc gtt cag       917
Thr Val Ala Phe Thr Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln
    125                 130                 135

caa atg ggt aaa atc gca acg gcg aat gcc ttg aaa aaa atc ttt cag       965
Gln Met Gly Lys Ile Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln
140                 145                 150                 155

ctc atc ggc ttg ttt tta ttt ttt caa tgg tat tcc ttt gaa ttg gat      1013
Leu Ile Gly Leu Phe Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp
                160                 165                 170

act tct ctt ctc att tca ttg ttt gtc ctc gtt gca agt gaa gtg gtc      1061
Thr Ser Leu Leu Ile Ser Leu Phe Val Leu Val Ala Ser Glu Val Val
            175                 180                 185

gtg ttt gtt tat ttg ttt tcg cag ttt gtt ttg gtc agg cgt gcc gct      1109
Val Phe Val Tyr Leu Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala
        190                 195                 200

caa aaa ggg cag cag atc cac ttg cgg aga aac gat gtt tta aaa cgc      1157
Gln Lys Gly Gln Gln Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg
    205                 210                 215

ctg ctc act gtt tcg atc ccg acg acg ggg ctg cgc gtg ttt cat gct      1205
Leu Leu Thr Val Ser Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala
220                 225                 230                 235
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gtg aca aat gcc gtc gaa cct ttt ttg gtg aag ggg acg ctg ctt gcc      1253
Val Thr Asn Ala Val Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala
        240                 245                 250

gct ggc gta tca aga aca tcg gcc atc gac cag ttc ggc atg ctt tcg      1301
Ala Gly Val Ser Arg Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser
    255                 260                 265

gga gtt gcg atg aca atc ggc ttt ttt ccg gct ttt atc gcc cat tca      1349
Gly Val Ala Met Thr Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser
    270                 275                 280

ctg atg gtc gtc atg atc ccg agc att tct gaa agc tac gct tac ggg      1397
Leu Met Val Val Met Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly
    285                 290                 295

caa tac gaa aga gtg atc aaa cgg att aaa cag gcg atc ttt att acg      1445
Gln Tyr Glu Arg Val Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr
300                 305                 310                 315

ctg ttt tac ggc ata ccg tcc gtc atg gtg atg tat cac ttt gca gag      1493
Leu Phe Tyr Gly Ile Pro Ser Val Met Val Met Tyr His Phe Ala Glu
                320                 325                 330

ccg ctg acc cat tta ttt ttc gat tcg gtc aag gcg tcg ttt tac ctt      1541
Pro Leu Thr His Leu Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu
            335                 340                 345

aaa atg ttg tgg ccg tat ttt tta ttc cac ttt ttt gcg atg cct ttt      1589
Lys Met Leu Trp Pro Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe
        350                 355                 360

cag gcc tgt tta atc gga atg ggg ttg gcc aaa gat gct ttt tat cat      1637
Gln Ala Cys Leu Ile Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His
    365                 370                 375

aac gtt tgg gcc agt gtc tta tcg ttt ttg atg atg tat gtt ctc ggg      1685
Asn Val Trp Ala Ser Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly
380                 385                 390                 395

tcc atg cag act ttg cag atg acg ggg atc att ctt gcg atg aat acc      1733
Ser Met Gln Thr Leu Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr
                400                 405                 410

ggt atg att ttg ctg acg gcg ctg cat tat gtg acg att tgc aag gag      1781
Gly Met Ile Leu Leu Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu
            415                 420                 425

ctg ggc gtc acg ctt ttt ttg aca aac aaa tcc cga tct ccg aga att      1829
Leu Gly Val Thr Leu Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile
        430                 435                 440

gaa agc cgc tgatggatcc tcttcatagt tttagctttt gcggggaagc              1878
Glu Ser Arg
    445

taatattaaa aaagaagggg agttcccatg cgaagaatca gtctcattta cccgctcatc   1938

ctgctgtttt ttaccgggtt attcgtattt cagccgcagg catctgcaaa acaagcttcg   1998

ccggcagtca tgcagatgaa cacggtcgaa ggtcagcgcg tcgtcattcc cgccgaaggc   2058

cagaagacga tcgttcattt ttggacgacc tggtgcccgc catgccgtga agagcttccg   2118

cgattccaat cctactatga aagcaagcaa tccggcgtca agctcgtgac cgttaattta   2178

ctgaatgccg aaaagaacga acagaaggta aaacagttta ttaaagcaaa caagctgaca   2238
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tttccgatcg tttttgacaa aaagggtgag atgatgaaag catataaagt catgacaatt 2298

cctacgactt ttttctttaa tgaaaaagga gagctggaga aaa 2341

<210> 115
<211> 446
<212> PRT
<213> Bacillus licheniformis

<400> 115

Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu Ser Leu Ala Ala Phe
1 5 10 15

Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met Ile Leu Ala Arg Glu
20 25 30

Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser Val Leu Pro Ser Ile
35 40 45

Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu Pro Val Ser Ile Ser
50 55 60

Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His Glu Ser Met Leu Lys
65 70 75 80

His Ala Leu Arg Met Thr Ala Val Cys Thr Val Phe Ser Thr Ala Ala
85 90 95

Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe Asp Ser Tyr His Pro
100 105 110

Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro Thr Val Ala Phe Thr
115 120 125

Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln Gln Met Gly Lys Ile
130 135 140

Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln Leu Ile Gly Leu Phe
145 150 155 160

Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp Thr Ser Leu Leu Ile
165 170 175

Ser Leu Phe Val Leu Val Ala Ser Glu Val Val Val Phe Val Tyr Leu
180 185 190

Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala Gln Lys Gly Gln Gln
195 200 205

Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg Leu Leu Thr Val Ser
210 215 220

Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala Val Thr Asn Ala Val
225 230 235 240

Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala Ala Gly Val Ser Arg
245 250 255

Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser Gly Val Ala Met Thr
260 265 270

Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser Leu Met Val Val Met
275 280 285

Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly Gln Tyr Glu Arg Val
290 295 300

Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr Leu Phe Tyr Gly Ile
305 310 315 320

Pro Ser Val Met Val Met Tyr His Phe Ala Glu Pro Leu Thr His Leu
325 330 335

Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu Lys Met Leu Trp Pro
340 345 350

Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe Gln Ala Cys Leu Ile
355 360 365

Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His Asn Val Trp Ala Ser
370 375 380

Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly Ser Met Gln Thr Leu
385 390 395 400

Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr Gly Met Ile Leu Leu
405 410 415

Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu Leu Gly Val Thr Leu
420 425 430

Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile Glu Ser Arg
435 440 445

<210> 116
<211> 1417
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (420)..(914)

<400> 116

cagcagctta ttttcgagcc gaaaccgctc catgatgctg atcccgcctc ctgctccctg 60

tgaggtgaca atcggaatgc ccgcctggtt gatcgcctca atatcccgat aaatcgttct 120

gacagagact tcgaacatgc cggcaagctc ctttgcctgc acttggcgtt tattaatcaa 180

taaatcaca atggccaaaa gccggtcaat tttcactgca gatccctcac attcatcttg 240

tgcagcctct tttttctgc tattttcatt ccatagcgca caccattctg ggatatcatg 300

acaaaaaaga ggatctcatc acccatttat ctagaaaacc acttttcagg ttacgatttg 360

tacagtttgg acatatactc cttaaaaaag gaggttttaa aaacatcata ttttatttt 419

ttg cag ttt ttc atc att gtg tcc atc gtc tat atc aag ttc aaa cgg 467
Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
1 5 10 15

tcg gtc ggt tat cag cct tta aag ccg gca cgc atg ttg ttc cgg atc 515
Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
20 25 30

atc ctt ttt tcg gga att ttc gtt ttt ctg ctg acg atg agc gca ctt 563
Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
35 40 45

cac cct tta tca tac ttt tat gat ctg att ggg atc gcg ctc gga ctc 611
His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
50 55 60

atc ttg acc gtc tat gcg ctg aag cat gtg tcg atc gaa aat cgg ggc 659
Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
65 70 75 80

gga gtc ctt tat ttc aga acg cat tta tgg gtt gaa ttg atc gta ctc 707
Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
85 90 95

ttt tta ttt tta tac cgg ttt ctg tac cgg atc gcc gag atc ggc cag 755
Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
100 105 110

ctg cag act gcg gtt tca gac ggg ggt tcg gca gct tac ggc gcc ctt 803
Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
115 120 125

ttt gcg cag gac ccg gcg acg atg atc ggt ttt ttt gta ctg gcc gtt 851
Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
130 135 140

tat tat gtc ggt ttc tct ttt ttt gtt tta aaa aaa ggc aga acc gaa 899
Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
145 150 155 160

gaa aag cgc tca gct taaaaaggca aactcgggaa attgagtttg ccttttaaac 954
Glu Lys Arg Ser Ala
165

tttagtcatg ttgtgtatga tcgatcatct gctgaagtac atcgaggaca tgctggtctt 1014

ccggagaata aaaaatggaa gtccctgccc ttcttgattt gacgagacga aggtttttta 1074

aaaacctgag ctggtgagaa acggttgact gcaggagact cagcttctct gctatttcat 1134

taaccgaatg ctcgccttgt gagagcaggt gaagaatttt gattctcgtt gggtcagaga 1194

gcgctttaaa cgtctgtgaa acgagaaata aagtttcttc atctaactcg gcccgcacct 1254

gtttttctgt tgtttcttga ttgtgctcac tcatgctttt cacctttttcc gcgcgacttt 1314

tacctccata tcatatacca aaacataccg gttgaaaagt tttaacggat caagtcgaaa 1374

acagcgttcc ttgaagcgct tctacatatc ttgcagcaga cct 1417

<210> 117
<211> 165
<212> PRT
<213> Bacillus licheniformis

<400> 117

Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
1 5 10 15

Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
20 25 30

Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
35 40 45

His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
50 55 60

Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
65 70 75 80

Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
85 90 95

Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
100 105 110

Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
115 120 125

Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
130 135 140

Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
145 150 155 160

Glu Lys Arg Ser Ala
165

<210> 118
<211> 2353
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1850)

<400> 118
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aaaggctgca cctaaacaag ccgcgcctaa aaaacaggat gccgttgcag ccaatatgcc 120
gggcggattc tcgaacaacg acattaatct gttggcccaa gcggtttacg gtgaagcgcg 180
cggagaaccg tatgacggcc aggttgccgt tgcagctgtt atattaaaca ggctcgatag 240
ccctacgttc ccgaatacgg tggcgggcgt tatctttgaa ccgcttgcat ttacagctgt 300
cgcggacgga cagatttata tgacgccgga tgaaacggcg aaaaaagccg ttcttgacgc 360
catcaacggc tgggatccat cagaaaatgc cacttactat tttaaccctg acacggccac 420
tagctcatgg atttggggca gacctcaaat taaaaggatc ggtaaacaca ttttctgtga 480
ataaaagcga ggtgctataa atg atc aga gga att tta atc gcc ctt tta ggt 533
Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly
1 5 10

gtc gcc atc gtc gga aca agc tat tgg ggc tat aaa gaa cat cag gag 581
Val Ala Ile Val Gly Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu
15 20 25

aaa gac gcc gtt ttg ctt cat gcc gaa aac aac tat caa agg gca ttt 629
Lys Asp Ala Val Leu Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe
30 35 40

cac gac tta act tat cag gtg gat cag ctg cat gat aaa atc ggg agc 677
His Asp Leu Thr Tyr Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser
45 50 55

acg ctt gcg atg aac agc aaa aaa acg ctg tct ccc gct ttg gcg gaa 725
Thr Leu Ala Met Asn Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu
60 65 70 75

gtc tgg aaa acg act tct gaa gcg cat aac aat gtc agc cag ctg ccg 773
Val Trp Lys Thr Thr Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro
80 85 90

ctg acc tta atg ccg ttt aac aag acc gaa gag ttt ttg gca aag gtc 821
Leu Thr Leu Met Pro Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val
95 100 105

gga gat ttc agc tac aaa gca gcc gtg cgc gat ctt gac aaa gag ccg 869
Gly Asp Phe Ser Tyr Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro
110 115 120

ctc aat aaa aaa gag tac gct tct tta aat cag cta tat gaa aat tca 917
Leu Asn Lys Lys Glu Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser
125 130 135

aag gat ata caa aat gaa ctg cgt aat gtc cag cat ttg att att gac 965
Lys Asp Ile Gln Asn Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp
140 145 150 155

aaa aat ttg aga tgg atg gat gta gaa ctt gcg ctc gcg tcc ggc caa 1013
Lys Asn Leu Arg Trp Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln
160 165 170

aaa caa agc gac aat aag att att aat ggc ttt aaa acc gtt gaa aaa 1061
Lys Gln Ser Asp Asn Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys
175 180 185

agc gca agt gca ttt tcg gat acg gat tta ggc gcg aca gag atg acg 1109
Ser Ala Ser Ala Phe Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr
190 195 200

aac acg aaa aaa gag cag caa ggg tac gac cat tta caa ggc aaa aga 1157
Asn Thr Lys Lys Glu Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg
205 210 215

ata acc gaa aaa gaa gcg cgc aag att gcc caa aaa ttc gcc cag gac 1205
Ile Thr Glu Lys Glu Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp
220 225 230 235

aaa aat tac aat atc aaa gta tcg aaa agc ggc aag aaa acg aac agg 1253
Lys Asn Tyr Asn Ile Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg
240 245 250

gat gta tac agc atc agt atg cag gac cct gat caa aaa gcg gat att 1301
Asp Val Tyr Ser Ile Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile
255 260 265

tat atg gac att acc gaa aaa ggc gga tat ccg gtt tat ctg att caa 1349
Tyr Met Asp Ile Thr Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln
270 275 280

aac aaa aaa att aaa gat gaa aaa atc agc tta aac gat gcg tca aac 1397
Asn Lys Lys Ile Lys Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn
285 290 295

aaa gcc ctt caa ttt ttg aaa aaa aac ggc tat aaa acg gaa gac ctg 1445
Lys Ala Leu Gln Phe Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu
300 305 310 315

aag atg gat gaa agc tcg caa tac gac ggc gtc ggg gtg ttt tca ttt 1493
Lys Met Asp Glu Ser Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe
320 325 330

gtt ccg gtc cag gac gat gtc tgg ctc tat ccg gac agc atc cgc atc 1541
Val Pro Val Gln Asp Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile
335 340 345

aag gtc gcg ctt gac gac ggc gag att acc ggg ttt aat gca aag gat 1589
Lys Val Ala Leu Asp Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp
350 355 360

ttc tta atc tcc cat aaa aaa aga gac ttg ccg aag ccc aaa cta acg 1637
Phe Leu Ile Ser His Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr
365 370 375

cct gaa aaa gcg aaa gca agc ctg aat ccc aac gta aaa gtt cag gag 1685
Pro Glu Lys Ala Lys Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu
380 385 390 395

acg cgc ctt gct tta gtc acg aac gag ctt tcg caa gaa gtg ctc tgc 1733
Thr Arg Leu Ala Leu Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys
400 405 410

tac gaa att ctc ggc acg att gaa aac gat aca ttc cgc atg ttc atc 1781
Tyr Glu Ile Leu Gly Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile
415 420 425

aat gcc aat gac ggc acg gaa gag aag gtt cag aaa atg aaa agc gca 1829
Asn Ala Asn Asp Gly Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala
430 435 440

gaa ccg ata tac aac gac ttg taaaaacgat agatcaaagg gaaaaggcga 1880
Glu Pro Ile Tyr Asn Asp Leu
445 450

taacatgcct tttccttttt agcattcgga ataattcgcc ctaaacattt ccatactgaa 1940

catatgggcg gaacgtccgc cggtaaattg aaaatgcccg gggccataaa ttttccgggc 2000

agcggaggaa taatatgaaa acaatcgaac ggttattatt taagatactc gtcgtacaga 2060

cggtcatttt aatcagcgtg cagcttcttt ttcatttctc caaggctgag ccttatctgt 2120

caaaggtcgt gcagtatgaa ggcgtgaaca acatgaaaat cggcgaatgg atcgagacat 2180

ttaagccgta attcacgcta aaatctcccc tttttcgcct aatacatgat acaatcctat 2240

aaggagtacc agatagcaag gagaggaatt atggaaaaga aattatgcat tgcaatagac 2300

ggccctgcgg cagccggaaa aagcaccgtg gcgaaaatcg tggccagaaa aaa 2353

<210> 119
<211> 450
<212> PRT
<213> Bacillus licheniformis

<400> 119

Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly Val Ala Ile Val Gly
1   5   10   15

Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu Lys Asp Ala Val Leu
            20   25   30

Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe His Asp Leu Thr Tyr
        35   40   45

Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser Thr Leu Ala Met Asn
    50   55   60

Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu Val Trp Lys Thr Thr
65   70   75   80

Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro Leu Thr Leu Met Pro
                85   90   95

Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val Gly Asp Phe Ser Tyr
            100   105   110

Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro Leu Asn Lys Lys Glu
        115   120   125

Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser Lys Asp Ile Gln Asn
    130   135   140

Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp Lys Asn Leu Arg Trp
145   150   155   160

Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln Lys Gln Ser Asp Asn
                165   170   175

Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys Ser Ala Ser Ala Phe
            180   185   190

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Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr Asn Thr Lys Lys Glu
        195                 200                 205

Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg Ile Thr Glu Lys Glu
    210                 215                 220

Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp Lys Asn Tyr Asn Ile
225                 230                 235                 240

Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg Asp Val Tyr Ser Ile
                245                 250                 255

Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile Tyr Met Asp Ile Thr
            260                 265                 270

Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln Asn Lys Lys Ile Lys
        275                 280                 285

Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn Lys Ala Leu Gln Phe
    290                 295                 300

Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu Lys Met Asp Glu Ser
305                 310                 315                 320

Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe Val Pro Val Gln Asp
                325                 330                 335

Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile Lys Val Ala Leu Asp
            340                 345                 350

Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp Phe Leu Ile Ser His
        355                 360                 365

Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr Pro Glu Lys Ala Lys
    370                 375                 380

Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu Thr Arg Leu Ala Leu
385                 390                 395                 400

Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys Tyr Glu Ile Leu Gly
                405                 410                 415

Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile Asn Ala Asn Asp Gly
            420                 425                 430

Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala Glu Pro Ile Tyr Asn
        435                 440                 445

Asp Leu
    450
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<210> 120
<211> 1355
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (249)..(1355)

<400> 120
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tatattgaaa accacagagg gcttttgctt ttcagcgata cggaagtaag gctgatgctc      120

aaacaggggc agtgcatcat tcaaggcaaa gactttgtca tcaaaacgat tttgcctgag      180

gaaattctgc ttgaaggcac gattgagctt gtccgctata tcgattcata agtcgggggg      240

aaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga aag atc cag       290
         Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln
         1               5                   10

ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat gaa tgc acc        338
Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr
15                  20                  25                  30

agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa gac gcc gtc        386
Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val
                35                  40                  45

ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg aag gtc atc        434
Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile
            50                  55                  60

aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa ggg ttt cct        482
Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro
        65                  70                  75

ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act ttt gga gtt        530
Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val
    80                  85                  90

gct gca ttt ttt atc atc atg ttc cta ttg tcc aac atg ctt tgg aaa        578
Ala Ala Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys
95                  100                 105                 110

att gat att aca gga gcc aat cca gag aca gaa cat caa atc aga cag        626
Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln
                115                 120                 125

caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag ttt tca atg        674
Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met
            130                 135                 140

ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg gtc gaa aac        722
Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn
        145                 150                 155

atc act tgg gtg ggc att gag tta aac ggt acc gcc ctt cac atg aaa        770
Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys
    160                 165                 170

gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc ggt ccg agg        818
Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg
175                 180                 185                 190
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cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa atg ttc gtg gaa      866
His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu
                195                 200                 205

aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa aaa ggg caa      914
Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln
            210                 215                 220

atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag caa aaa gtc      962
Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val
        225                 230                 235

gga gca aaa ggg aaa atc tat ggt gaa acc tgg tac aag tca aca gta      1010
Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val
    240                 245                 250

acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt aaa gta agg      1058
Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg
255                 260                 265                 270

aca agt cac aag cta tcc ctc gga tca tta acc atg ccg atc tgg ggc      1106
Thr Ser His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly
                275                 280                 285

ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg gag acc gaa      1154
Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu
            290                 295                 300

aaa cac tcg ctg cat ttt ata aat ttt aag ctt cct gtc gct tat gaa      1202
Lys His Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu
        305                 310                 315

aag gag cat atg agg gag agc gaa caa atc aaa agg gtg tac tcg aaa      1250
Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys
    320                 325                 330

aaa gaa gca gtt ctt aga agg aat cga aat ggg aaa aag aga cat cag      1298
Lys Glu Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln
335                 340                 345                 350

gac aaa aat cgg cag aga cgg gaa cat tat cag tgt aaa agt ttt gca      1346
Asp Lys Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala
                355                 360                 365

cac cac gag                                                           1355
His His Glu
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<210> 121
<211> 369
<212> PRT
<213> Bacillus licheniformis

<400> 121

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Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln Leu Lys
1               5                   10                  15

Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Arg Arg
            20                  25                  30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val Phe Leu
        35                  40                  45
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Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly
50 55 60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu
65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
85 90 95

Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln Gln Leu
115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu Lys Gly
195 200 205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
260 265 270

His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly Phe Ser
275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Lys His
290 295 300

Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu
305 310 315 320

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu
325 330 335

Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln Asp Lys
340 345 350

Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala His His
355 360 365

Glu

<210> 122
<211> 2120
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1625)

<400> 122
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ttaccaagat ctcggcttaa aggcgacaaa gctgacaaag gaaaaagcaa tcgacgaagg 120

cccgggctac acgagcattt ccttagaaaa gctgcctgat ttcgctggag attatatatt 180

tataggacct tgggaatcaa gcggagacga cagcgccgtg cttaatacat ccatttggaa 240

gaaccttggg gcggtcaaaa accaacatgt ctataaaatc gaccctgtcg gcttctattt 300

ttccgatccg atttcattag agggccagct cgaatttatt acagaaaact taacaaaata 360

gaagaacttc cgccttgtca ggcggaagtt ttttttgcgc gcgaaaccgg ggtgaaccct 420

cattgaaaaa gcgattttca agtgcaagcc gggagagttt ttaaacgagc attcctcata 480

tgctattgtg ggagggatca ttg atg gca ttc atc aac atc aaa ccg gag tta 533
Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu
1 5 10

aag cag aat atg gaa aga ctg tct gac att ctg aac ata ccc gaa ccg 581
Lys Gln Asn Met Glu Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro
15 20 25

ctt tta atc agt gca aat gca aat gta tcc gcg gac gaa ctt tat ttt 629
Leu Leu Ile Ser Ala Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe
30 35 40

ccg gga gta tct ttt cat gca gga aaa aac gtt caa gca gca gaa aca 677
Pro Gly Val Ser Phe His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr
45 50 55

tat gaa cag ctg caa tta ttg gcg aat caa tac acg ttt gaa gat gaa 725
Tyr Glu Gln Leu Gln Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu
60 65 70 75

cag tgg ctg aca aaa aca gcc gtt tac gat tca gca gaa ctg aaa aag 773
Gln Trp Leu Thr Lys Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys
80 85 90

gaa att ggc aga ttg acg gaa tgc ttt ccg ttt gtt act tcc cgt atc 821

Glu Ile Gly Arg Leu Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile
95 100 105

atc ggc cgc tca agc atg ggc cag cct ata tat gaa ctg ctc ctt gga 869
Ile Gly Arg Ser Ser Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly
110 115 120

gct gaa aat gcc gga aaa aga acg cat atg aat gcc tct ttt cat gcc 917
Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala
125 130 135

aat gaa tgg atc acc act tct gtt ttg atg aaa tgg ctc aaa gaa tac 965
Asn Glu Trp Ile Thr Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr
140 145 150 155

tgt tat cat tta tgt aca ggc cag acc gct tta ggt ttt tcg ccg ctc 1013
Cys Tyr His Leu Cys Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu
160 165 170

gat att ttt tca tca aca aag ctt tcc gtc gtg ccg atc gtt aat ccc 1061
Asp Ile Phe Ser Ser Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro
175 180 185

gac ggt gtt gac ctt gta ctt aac ggc ccc ggt cat ctt ggg atc gcg 1109
Asp Gly Val Asp Leu Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala
190 195 200

aga gaa gcg ctg gat gag atg aac gag cat cag ccg gat ttc cgg gaa 1157
Arg Glu Ala Leu Asp Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu
205 210 215

tgg aaa gcc aat ata aac gga gtg gat tta aat aat cag ttt ccg tct 1205
Trp Lys Ala Asn Ile Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser
220 225 230 235

ttc tgg gag atc gaa aaa caa aga aaa ccg cct aaa tcc cct tcc tac 1253
Phe Trp Glu Ile Glu Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr
240 245 250

aga gac tac ccc gga gat gaa ccg ctg aca gaa ccg gaa gcg gca gcg 1301
Arg Asp Tyr Pro Gly Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala
255 260 265

atg agg gat tta atc gca aac gag ccg cct gac cgg ctt gtg gcg ctt 1349
Met Arg Asp Leu Ile Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu
270 275 280

cac aca cag ggg gag gaa att tat tgg gga tac aag gga ttg gag cct 1397
His Thr Gln Gly Glu Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro
285 290 295

cct gaa tca gct gat gtg atc caa aca ttt gag cgc ctg agc ggt tat 1445
Pro Glu Ser Ala Asp Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr
300 305 310 315

aag ggc gtc aga tat ata gac agc tat gca gga ttt aga gat tgg ttt 1493
Lys Gly Val Arg Tyr Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe
320 325 330

att cat tat tac gga aga gaa gga tat act gtt gaa ctt ggc aaa gga 1541
Ile His Tyr Tyr Gly Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly
335 340 345

aaa aat cct tta ccg ctg aaa caa ttt gac gat ata tat tgt aaa agc 1589
Lys Asn Pro Leu Pro Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser
350 355 360

aga gga ata ctt tgg gca tcc tgt ttt ttt gaa agc tgaaactttt 1635

Arg Gly Ile Leu Trp Ala Ser Cys Phe Phe Glu Ser
365 370 375

cacggtgaaa atcgtaaatt agacagccaa acatttatgg agggagaatg gccggtttga 1695

gagtttcatt attgattatt gccgctctga tggccgtggc tgcggctggt tgcacgccgc 1755

agcatcaaga aggatcaaaa agcgttcatc atgaggagcc ggaagggaaa agagaaagcg 1815

gtgcagcagt aaaagataaa aaagtgatag cgctgaagga ccggcacttt gatgagacgg 1875

caggatggct tgataatgaa accgttatat acaccgcaac cgatccggtc ggaggaagtg 1935

aaatcaaatc atatgatata tttaaaggga cgggcaaaac gatctacaag acagatgaca 1995

ggctgatagc gtcggaagtc aacagtgaaa aaggcatgat tcttatccaa accgccggaa 2055

acggctctga aatgaagtta actttgctta atttacaggg gaaacagctg tttgcaaaaa 2115

aattt 2120

<210> 123
<211> 375
<212> PRT
<213> Bacillus licheniformis

<400> 123

Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu Lys Gln Asn Met Glu
1 5 10 15

Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro Leu Leu Ile Ser Ala
20 25 30

Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe Pro Gly Val Ser Phe
35 40 45

His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr Tyr Glu Gln Leu Gln
50 55 60

Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu Gln Trp Leu Thr Lys
65 70 75 80

Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys Glu Ile Gly Arg Leu
85 90 95

Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile Ile Gly Arg Ser Ser
100 105 110

Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly Ala Glu Asn Ala Gly
115 120 125

Lys Arg Thr His Met Asn Ala Ser Phe His Ala Asn Glu Trp Ile Thr
130 135 140

Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr Cys Tyr His Leu Cys
145 150 155 160

Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu Asp Ile Phe Ser Ser
165 170 175

Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro Asp Gly Val Asp Leu
180 185 190

Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala Arg Glu Ala Leu Asp
195 200 205

Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu Trp Lys Ala Asn Ile
210 215 220

Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser Phe Trp Glu Ile Glu
225 230 235 240

Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr Arg Asp Tyr Pro Gly
245 250 255

Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala Met Arg Asp Leu Ile
260 265 270

Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu His Thr Gln Gly Glu
275 280 285

Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro Pro Glu Ser Ala Asp
290 295 300

Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr Lys Gly Val Arg Tyr
305 310 315 320

Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe Ile His Tyr Tyr Gly
325 330 335

Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly Lys Asn Pro Leu Pro
340 345 350

Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser Arg Gly Ile Leu Trp
355 360 365

Ala Ser Cys Phe Phe Glu Ser
370 375

<210> 124
<211> 1597
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (342)..(1094)

<400> 124

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aaagcgatgg tcatctcaaa actgtaacca attattttct tgatagtgtg gctgcgacta       120

ttatgcgctg attgtttacg gtgcttgctt tttataccat tggttcattt gaccggaatc       180

gtgttttgat tgcaggaatt tttgttactg tttgtgaaaa aacagcagaa gaaaaacagc       240

ggaaaactcg cgtcttaggg cggatttcca aaaaaatgtc gtaaattcga tgcatcaatt       300

tgatgaaatc gcccggccat gcggtataat agattttgtg a atg aaa gat tca atg       356
                                              Met Lys Asp Ser Met
                                              1               5

ttg aaa gag agt ggt tac atc atg ggc cgt aaa tgg aac aat ata aaa         404
Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys Trp Asn Asn Ile Lys
                10                  15                  20

gag aag aaa gcg tcc aag gat gcg aat acg agc cga atc tac gcg aag         452
Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser Arg Ile Tyr Ala Lys
            25                  30                  35

ttc ggc cgc gaa atc tat gtg gcg gca aag cag gga gag ccc gat ccc         500
Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln Gly Glu Pro Asp Pro
        40                  45                  50

gaa ctg aac cag aac ctg aaa ttc gtg ctt gag cgc gcc aaa aca tac         548
Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu Arg Ala Lys Thr Tyr
    55                  60                  65

aat gtc ccg aaa gcg att att gag cgg gcg atc gaa aaa gcg aag ggc         596
Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile Glu Lys Ala Lys Gly
70                  75                  80                  85

ggc tct gag gaa aat tac gac gag ctg cgc tat gaa ggc ttc ggt ccg         644
Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr Glu Gly Phe Gly Pro
                90                  95                  100

aac gga gcg atg gtg atc gtt gac gcg ttg aca aac aac gtc aac cgc         692
Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr Asn Asn Val Asn Arg
            105                 110                 115

acg gct gcc gat gtg cgc tcc aca ttt ggc aaa aac ggc gga aac atg         740
Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys Asn Gly Gly Asn Met
        120                 125                 130

gga gtg agc gga tct gtc gct tac atg ttt gat ccg acg gcc gtc atc         788
Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp Pro Thr Ala Val Ile
    135                 140                 145

ggc ttt gaa ggc aaa acg gct gat gaa acg ctc gaa tta ttg atg gaa         836
Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu Glu Leu Leu Met Glu
150                 155                 160                 165

gcg gat atc gat gtc cgt gat att tta gag gaa gac gat gca gtg atc         884
Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu Asp Asp Ala Val Ile
                170                 175                 180

gtc tat gcc gag ccc gat cag ttc cac gcc gta cag gag gcg ctg caa         932
Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val Gln Glu Ala Leu Gln
            185                 190                 195

aac gcc ggc att act gag ttc acg gtg gcc gag ctg acg atg ctc gcg         980
Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu Leu Thr Met Leu Ala
        200                 205                 210

caa aat gac gtc gcc ctt cca gag gac gcg cgc gca cag ttt gaa aag        1028
Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg Ala Gln Phe Glu Lys
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215 220 225

ctg att gac gcg ctg gaa gat ctg gaa gac gtt cag caa gtt tac cat 1076
Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val Gln Gln Val Tyr His
230 235 240 245

aat gtc gat tta ggg gcg taaaaagagg ccctgaaaaa atcgggaaag 1124
Asn Val Asp Leu Gly Ala
250

aaaagataga tgaacaggag gacgacctgt tttgtctatc ttttttatt gtaaagttaa 1184

cttgacattt tatttttttg ttaagtatac tttacgtata gtgaacttta cattcccaat 1244

ggaggaaaga tgaaaacgtt aataaaggaa aagcgcactt cgctgaacat gacacaagaa 1304

gaactggcta aaaggcttaa tgtgtcgagg caaacggtga tttcccttga aaagggaaaa 1364

tataaacctt cactcgttct ggcgcataaa ctggctcaaa tttttgaatg tctgattgaa 1424

gatttattta tttttgaggg ggatgaaaat attgactgaa acgatgacaa acatactgat 1484

cgctttagcg ggcttagaat aggcgtgctc gggatcgcaa ttgtttacaa agtaaacaga 1544

cgaattggaa aaaaagagag gctgttcgat gagcgccagc agaagattag cta 1597

<210> 125
<211> 251
<212> PRT
<213> Bacillus licheniformis

<400> 125

Met Lys Asp Ser Met Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys
1 5 10 15

Trp Asn Asn Ile Lys Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser
20 25 30

Arg Ile Tyr Ala Lys Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln
35 40 45

Gly Glu Pro Asp Pro Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu
50 55 60

Arg Ala Lys Thr Tyr Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile
65 70 75 80

Glu Lys Ala Lys Gly Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr
85 90 95

Glu Gly Phe Gly Pro Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr
100 105 110

Asn Asn Val Asn Arg Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys
115 120 125

Asn Gly Gly Asn Met Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp
130 135 140

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Pro Thr Ala Val Ile Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu
145                 150                 155                 160

Glu Leu Leu Met Glu Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu
                165                 170                 175

Asp Asp Ala Val Ile Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val
            180                 185                 190

Gln Glu Ala Leu Gln Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu
        195                 200                 205

Leu Thr Met Leu Ala Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg
    210                 215                 220

Ala Gln Phe Glu Lys Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val
225                 230                 235                 240

Gln Gln Val Tyr His Asn Val Asp Leu Gly Ala
                245                 250


<210>  126
<211>  1888
<212>  DNA
<213>  Bacillus licheniformis


<220>
<221>  CDS
<222>  (3)..(1385)

<400>  126
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   Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile
   1               5                   10                  15

att gct ttc tcc att cta tat ttg tcc gcc ccg ttt ttt gca gag atg      95
Ile Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met
                20                  25                  30

gcc ctt ggc gga aca gaa aac aac ggg ctg acg ctt gaa cat gtc gtg     143
Ala Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val
            35                  40                  45

tat gtc att cgc atg gtc agt ctc gcg cta ctg gtt gtg ccg atc ttg     191
Tyr Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu
        50                  55                  60

gcg ctg atc aga ggc ttt ttc caa ggt cac cag atg atg ggg ccg aca     239
Ala Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr
    65                  70                  75

gcc gtt tca cag gta gtt gaa caa att gcc aga atc gtc ttt cta tta     287
Ala Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu
80                  85                  90                  95

acg gcc act tac ttg gtg atc aaa gta tta aac ggc ggg ctt gtc gtc     335
Thr Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val
                100                 105                 110
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gct gtc ggc tat gcg act ttt gcg gct ttg atc gga gcg ttc gcc gga 383
Ala Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly
115 120 125

ctg ttc act ctt tac ttt tcc tgg cag aaa aga aaa ggg gcg ctc ctg 431
Leu Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu
130 135 140

gcg ctg aag ccg aac ctt gtt cct tca gcc gat att acg tac cgg caa 479
Ala Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln
145 150 155

atg ttt aaa gag ctg ttc agc tat gcc gcc cct tat gtc ttt gtc ggg 527
Met Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly
160 165 170 175

ctg gcg ata ccg ctt tac cag tac att gat acg aat acg ttt aat aaa 575
Leu Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys
180 185 190

gcg atg att gca gcc ggc tat caa aac atc agc cag gat ttg atg gcg 623
Ala Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala
195 200 205

atc gtg acg ctg tac gtg cca aag ctt gtg atg att ccg gta tct ctc 671
Ile Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu
210 215 220

gcg acg gca ttc ggg ctg aca ttg att ccg gcg gtg act gaa aac ttt 719
Ala Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe
225 230 235

acc aac aaa gat ttc cct gct tta aac aaa cag att gat cag gcg atg 767
Thr Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met
240 245 250 255

cag atc att ctc ttc atc gtt ctt ccg gca tca gtc ggt atg gct ctt 815
Gln Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu
260 265 270

ttg tcg ggg ccg gtt tac acg ttc ttt tac ggc tcg gaa agc ctg ctc 863
Leu Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu
275 280 285

cct gac atg gga cga gat att ttg ttc tgg tac gcg cct gtg gcg ctg 911
Pro Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu
290 295 300

tta ttc tcg ctc ttc acc gtc aac gct gca att ttg cag ggg gtg aac 959
Leu Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn
305 310 315

aag cag aaa ttt gcg gtt gtc agc ttg atg atc ggg att gtg atc aaa 1007
Lys Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys
320 325 330 335

atc gcg ctt aac gtt ccg ctc atc aag ctg ctt caa ggc agc ggg tcg 1055
Ile Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser
340 345 350

att ttg gca acg gcg ctc ggc tat tca gct tca ctc cta tac gga ttt 1103
Ile Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe
355 360 365

atc atg att aaa cgc cat gcc ggc tat tcg tat cgc aaa ctg ttt aaa 1151
Ile Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys
370 375 380

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cgg ttt ttg ctg atg ctg atc ctg acg gcg gtc atg ggc atc att ttg      1199
Arg Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu
    385                 390                 395

ctg ctt gtc cag gcg ctt cta agt att ttt att tca tac gaa ggc ggg      1247
Leu Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly
400                 405                 410                 415

cag atc agg tct gct gtc gtc att ttc atc aca acc gca gtg ggc ggg      1295
Gln Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly
                420                 425                 430

tca gtt tat ctg tac ttg gct tac cgt gtg aaa ctg ctc gaa aaa atc      1343
Ser Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile
            435                 440                 445

ttc ggt cag cga ttg aat cgc ttt ttc aaa aga aag gcc tcc              1385
Phe Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
        450                 455                 460

taaaaagggc ttttcttttt atgtaaaaaa aggggtgtct tcatgagatt ggataaactg   1445

ttgtcaaaca gcggctatgg ttcgagaaaa gaagtcaaaa aaatgctgaa aaacggcgcg   1505

gtgcgcgtca atgatcaatt agtcaaagac gccaaaaagc acgttgaccc ggaatcagac   1565

gacatcacgg tatacggggc acccgtcatg taccgggaat ttatttactt aatgatgaac   1625

aagccgcaag gagtgctgtc agcaacagaa gacagccggc aggaaacggt tgtcgatttg   1685

ctcgacccgg agctgctgag gtttgagccg tttcctgtcg gaaggcttga caaggatact   1745

gagggactgc tgcttctgac gaatgacgga cagttggcac accagctttt atctccgaaa   1805

aaacacgtac ctaaaacgta tgaagtccat gtcaataagc cgattgatca agcggcactt   1865

gatcagcttg aaaaaggggt cga                                            1888

<210>  127
<211>  461
<212>  PRT
<213>  Bacillus licheniformis

<400>  127

Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile Ile
1               5                   10                  15

Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met Ala
            20                  25                  30

Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val Tyr
        35                  40                  45

Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu Ala
    50                  55                  60

Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr Ala
65                  70                  75                  80

Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu Thr
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85 90 95

Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val Ala
100 105 110

Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly Leu
115 120 125

Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu Ala
130 135 140

Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln Met
145 150 155 160

Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly Leu
165 170 175

Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys Ala
180 185 190

Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala Ile
195 200 205

Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu Ala
210 215 220

Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe Thr
225 230 235 240

Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met Gln
245 250 255

Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu Leu
260 265 270

Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu Pro
275 280 285

Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu Leu
290 295 300

Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn Lys
305 310 315 320

Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys Ile
325 330 335

Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser Ile
340 345 350

Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe Ile

355 360 365

Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys Arg
370 375 380

Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu Leu
385 390 395 400

Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly Gln
405 410 415

Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly Ser
420 425 430

Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile Phe
435 440 445

Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
450 455 460

<210> 128
<211> 1852
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1349)

<400> 128
tcacttttttg aatcagctgt cagacgcttt gaagctggaa aacacagctt tttaccatga 60

ccgcgcggaa acattcggaa gatcgaaaga ccacagagaa agctatgacg ttgtgacggc 120

acgcgctgtc gcccgccttt cggttctcag cgagctctgc cttccgcttg tgaaaaaaga 180

cggtttattc gtagcattaa aagccgcttc ggctgatgaa gaaattgaaa cgggcaaaaa 240

agccatcaaa acgcttggag gcaaaattga aaccgtacat tcttttcagc tgccaataga 300

agaaagcgaa agaaacatca ttgtcatcaa aaaacaatcg cagacaccga agaaatttcc 360

aagaaagcct ggaacaccta ataaatctcc tattgaaggt taaattattc gttttcttca 420

aatttcgtga tgtcacagaa ggaaaattca tgagaaaata gaattataaa aatggcagtg 480

tttaaaggtg gtgtaggtac atg aag cat tca ttc tct cgt ctc ttc gga ctt 533
Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu
1 5 10

ggc gac aag gaa gaa gaa gca gag att gct gaa cat gat acg aat aaa 581
Gly Asp Lys Glu Glu Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys
15 20 25

gaa gaa att caa gag att cca gta ggc gat ata att cct aac cgt ttt 629
Glu Glu Ile Gln Glu Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe
30 35 40

cag ccg cgc acc att ttc tca gaa gaa aaa att aaa gaa tta gct gca 677
Gln Pro Arg Thr Ile Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala

45 50 55

acc att cat aca cac ggc att atc cag ccg att gtc gtc aga aaa aca 725
Thr Ile His Thr His Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr
60 65 70 75

gag cgg gaa ggc caa tat gaa ctc ata gcc gga gag cgg cgc tgg cgg 773
Glu Arg Glu Gly Gln Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg
80 85 90

gcg gtt caa acg ctc gat tgg gag aag gtt ccc gct att att aag gat 821
Ala Val Gln Thr Leu Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp
95 100 105

ttt tca gat aca gag acc gct tct gtc gct ctt atc gaa aac ctt cag 869
Phe Ser Asp Thr Glu Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln
110 115 120

agg gaa gaa tta tct tcg att gaa gag gcg cat gct tat gca agg ctt 917
Arg Glu Glu Leu Ser Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu
125 130 135

tta gag ctt cac gat ttg acg cag gaa gcc ctt gca caa agg ctt gga 965
Leu Glu Leu His Asp Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly
140 145 150 155

aag ggc cag tca aca atc gcc aat aag ctc aga ctg tta aag ctt ccg 1013
Lys Gly Gln Ser Thr Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro
160 165 170

gaa gag gtg cag gaa gcg atc ttg aaa aaa gaa att tca gag cgc cac 1061
Glu Glu Val Gln Glu Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His
175 180 185

gca aga gcg ctc ata ccg ttg aaa cag ccc gac ctt cag gtc aag ctg 1109
Ala Arg Ala Leu Ile Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu
190 195 200

ctg cat gaa gtc att gaa aag agt tta aat gta aaa caa acc gaa gac 1157
Leu His Glu Val Ile Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp
205 210 215

cgt gtc gtc aaa atg ctt gag cag gat aaa cgc aag cct aaa cca aag 1205
Arg Val Val Lys Met Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys
220 225 230 235

aga aaa gcg tac agc agg gac gcg aga atc gcg atg aat acg att cgc 1253
Arg Lys Ala Tyr Ser Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg
240 245 250

cag tcc tta tca atg gtg gaa gac agc ggc gtc aaa ctg aat acg gaa 1301
Gln Ser Leu Ser Met Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu
255 260 265

gaa gag gaa ttt gaa gaa tat att cag ttt acg att cga ata ccg aaa 1349
Glu Glu Glu Phe Glu Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
270 275 280

taaaagctcc ctatagagct tttatttttt taggcaaaat atctatgggg gagcgtctat 1409
ggaatattat cgacaatatc attcattgct tttttcgatt gcttaccgta tgctcgggtc 1469
ttttcaagat gcagaggaca tcatccaaga attgttcgca gaccttcagg aaaaagatat 1529
cggtcaaatt gaccatattc aagcatattt aacgaaatca atcacaaacc gctgcataaa 1589
tgaactgcag tctgcccgca agaagcggga ggtatatatc ggggaatggc ttccggaacc 1649

gcaggtggcg ctttcagctc aaatcccggc tgagtacgtt gaagagaaag aaaaggtatc 1709

ctatgctttt ctggtagtta tgagccgatt aaatcctgta gaaagagccg ttttgatgtt 1769

tagagaagta tttggatatc attacaagga aatttcgtcc attatcggga agtcggaagc 1829

gaactgtcgt caaatccaca gcc 1852

<210> 129
<211> 283
<212> PRT
<213> Bacillus licheniformis

<400> 129

Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu Gly Asp Lys Glu Glu
1 5 10 15

Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys Glu Glu Ile Gln Glu
20 25 30

Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe Gln Pro Arg Thr Ile
35 40 45

Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala Thr Ile His Thr His
50 55 60

Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr Glu Arg Glu Gly Gln
65 70 75 80

Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Val Gln Thr Leu
85 90 95

Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp Phe Ser Asp Thr Glu
100 105 110

Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln Arg Glu Glu Leu Ser
115 120 125

Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu Leu Glu Leu His Asp
130 135 140

Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly Lys Gly Gln Ser Thr
145 150 155 160

Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro Glu Glu Val Gln Glu
165 170 175

Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His Ala Arg Ala Leu Ile
180 185 190

Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu Leu His Glu Val Ile
195 200 205

Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp Arg Val Val Lys Met
210 215 220

Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys Arg Lys Ala Tyr Ser
225 230 235 240

Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg Gln Ser Leu Ser Met
245 250 255

Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu Glu Glu Glu Phe Glu
260 265 270

Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
275 280

<210> 130
<211> 1495
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(995)

<400> 130
gcagacctga ctacgaaggc atcctgtcaa agctgagcaa aaaagccttt tcgattttgc 60

tcgtccatga gcctgatgcc gctttaacgg caaatcaata ccccgtcaat ctgcaaatat 120

ccggacacac ccacgcgcgg acaaattcag attcctgtat tcggtccttt gattacgcct 180

ccgtacgtag acgtttatac gcaaggaatg tatgcaacag ccggaatgaa aatttatgtc 240

atttgaggaa tcggcacgag caggctgccg ctccgctttc tgtcaaagcc tgaaatcacc 300

gtgttccagc ttgaatccat ttaatcttgc ccggtccttt ggctcaaaac aaaaggcatc 360

tgcatacatt aagtaaaaac attcccgctc catttcatcc aatcccatca aaaaaacgga 420

acttcctcag cctcttccgt ctatatatta gcagcggaaa aggctctctt ttcgtttttg 480

aaaaggagat gtgctgatta ttg ctg atg tac caa gtc aaa ccc gga gga acc 533
Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr
1 5 10

ctt gaa agc atc gcc gcc gat ttc aga acg acc cgg cag gcg ttg ctg 581
Leu Glu Ser Ile Ala Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu
15 20 25

cag gcg aat cct ggc tta aac ggc ggc caa gtg tcc gcg ggc cag tcg 629
Gln Ala Asn Pro Gly Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser
30 35 40

att atc att ccc ggc atc aga aat ccg gac aca att cca tac cgg att 677
Ile Ile Ile Pro Gly Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile
45 50 55

gcc gtg tct ctc aac gga aga acg ctc aga ttg tat gag cga gac aga 725
Ala Val Ser Leu Asn Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg
60 65 70 75

ctt gta aaa aca tat ccg att gcc gtc gga aaa atc ctc aca cag acg 773

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Leu Val Lys Thr Tyr Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr
                80                  85                  90

ccg aga ggc gaa ttt gtc atc gtc aac cgg cag cca aat ccg ggc ggc        821
Pro Arg Gly Glu Phe Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly
            95                  100                 105

ccg ttc ggc gcc tac tgg ctg agc ctg tca aaa cag cac tac ggc atc        869
Pro Phe Gly Ala Tyr Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile
        110                 115                 120

cat gga acg aat aac cct tcg tca att ggc aaa gct gtt tca agg gga        917
His Gly Thr Asn Asn Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly
    125                 130                 135

tgt atc cgc atg cac aat cgg gat gtt ctg gaa ctt gct tct atc gta        965
Cys Ile Arg Met His Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val
140                 145                 150                 155

ccc aac gga acc cga gtg tcc att aca cct tagacgagta catttccaga         1015
Pro Asn Gly Thr Arg Val Ser Ile Thr Pro
                160                 165

caaatgcaat ttgaacaata caacatcttg tattaagata taatgggacc tttagggtaa     1075

ggagcgtata tatggatctt tttaaaaatc gtaatttcgt ccgacttttt ttcgcagctt     1135

tcgcttctca aatgggaacg acagtcggaa atatggcttt cgccttttttc ttgctcgacc    1195

ggttcagcag ccagccggcc tatacgacaa tcgccgagct gatgtattcc ttgccgacgg     1255

ttttcgtatt ctttatcgtc ggggtggtcg ctgaccgttt tgaccgcaag aaagtcgcgg     1315

aaaactgtga ttggatcaga ggcgggactg actgtcgttc ttttctttgt attgtatctt     1375

caaattatac cgcttgtgtt tttagtccta tttatcagaa gcgcggttac aaaatttttc     1435

tacccggccg aagcaagttt ggtccaggcc attttaagaa aggaccagta tgcaaaggct     1495


<210>  131
<211>  165
<212>  PRT
<213>  Bacillus licheniformis

<400>  131

Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr Leu Glu Ser Ile Ala
1               5                   10                  15

Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu Gln Ala Asn Pro Gly
            20                  25                  30

Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser Ile Ile Ile Pro Gly
        35                  40                  45

Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile Ala Val Ser Leu Asn
    50                  55                  60

Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg Leu Val Lys Thr Tyr
65                  70                  75                  80

Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr Pro Arg Gly Glu Phe
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85 90 95

Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly Pro Phe Gly Ala Tyr
100 105 110

Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile His Gly Thr Asn Asn
115 120 125

Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly Cys Ile Arg Met His
130 135 140

Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val Pro Asn Gly Thr Arg
145 150 155 160

Val Ser Ile Thr Pro
165

<210> 132
<211> 1897
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1397)

<400> 132
tttccatcgc ggtgcagttt tatacggagg ccaaaacggt catgaatgta ccaaagaccg 60

tatttgtccc tcagcctaac gtagattccg cggtcatcag gctgacgctg aggaaagagc 120

cggctgtggc cgttcaagat gctgcctttt tctttcaagt cgtaaaagca agctttgcac 180

agcgtcgaaa aacgcttttc aacaacctcg tcaacaatct gccgaatggc aaagagaata 240

aatcaaaaat tgaaagagcg cttcaggatt cacatatcga cggaaaacga cgcggagagt 300

cgcttagcat tgaagagttc gccgtcttat ctgaccgctt gagagaagtc cttctttaat 360

ggagggcttt ttttattgat gccgggcttt aagcctgatc aggcttgtca tccgttcacc 420

acttgaaggg caggcacata ggctaaagaa gcacctttac tttttcgttg cttgatgttc 480

atcaggatgg ggcttagtct atg tgt gga gtg aaa agc atg caa ttt aaa ata 533
Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile
1 5 10

ggc gat atg gtc gtc aga aaa tct tat cga aga gat att tta ttt cga 581
Gly Asp Met Val Val Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg
15 20 25

att ata aga att gat caa tcg gca aat gga gaa cct gta gcc gtt ttg 629
Ile Ile Arg Ile Asp Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu
30 35 40

cac gga gat gag gtc aga tta atc gct gac gcg cat ttg ggg gat ctt 677
His Gly Asp Glu Val Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu
45 50 55

gag att gtc cgc gag gct gag tgg cag atg aga aag cgg gaa gaa gaa 725
Glu Ile Val Arg Glu Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu

60 65 70 75

acg aga atg aag gaa tcc ctc gat ctt ctc cgc cag gat tac aaa ctc 773
Thr Arg Met Lys Glu Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu
80 85 90

ctt cac gat aaa cat gag tac cgc gcc aca aac caa tat aac aat caa 821
Leu His Asp Lys His Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln
95 100 105

cag cag tac ttt cat atg ccc gga aga gtc ctt cat tta gac ggg gat 869
Gln Gln Tyr Phe His Met Pro Gly Arg Val Leu His Leu Asp Gly Asp
110 115 120

tcg gct tat ttg aaa aag tgt ctg gcg ctc tac gaa aag atc ggg gtt 917
Ser Ala Tyr Leu Lys Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val
125 130 135

cct gta tac ggc att cat tgc tat gaa aag aaa atg tca tca gtc atc 965
Pro Val Tyr Gly Ile His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile
140 145 150 155

gag gaa ctg atc gat gaa tac cgc ccg gat ctt ctc gtc att acc gga 1013
Glu Glu Leu Ile Asp Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly
160 165 170

cac gat gcc tat tct aag cag aag ggc gat att aac aat ctg gat gcc 1061
His Asp Ala Tyr Ser Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala
175 180 185

tac agg cat tca aaa gat ttt atc gaa acc gtt caa aaa gcg aga aga 1109
Tyr Arg His Ser Lys Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg
190 195 200

aaa att ccc cat ctt gat cag ctc gtc att ttt gcc ggc gca tgc cag 1157
Lys Ile Pro His Leu Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln
205 210 215

tcc cat ttt gaa tca ctg atc aga gcc ggt gca aat ttc gca agc tct 1205
Ser His Phe Glu Ser Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser
220 225 230 235

ccg tcc aga gtc aac atc cat gcg ctt gat ccg gtc tat ata gtc gca 1253
Pro Ser Arg Val Asn Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala
240 245 250

aaa atc agc ttc act ccg ttt atg gac cgc att aac gtc tgg gaa gtg 1301
Lys Ile Ser Phe Thr Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val
255 260 265

ctc aga aat acc ttg acg aga gaa aag ggg ctc gga ggt att gag acg 1349
Leu Arg Asn Thr Leu Thr Arg Glu Lys Gly Leu Gly Gly Ile Glu Thr
270 275 280

cgg ggc gta ttg cgt att gga atg cca tat aaa aca aaa gca aac gat 1397
Arg Gly Val Leu Arg Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp
285 290 295

taaacgagcc cgccggatgg cgggtttttg ctatgcacac gaaatgtttt tacctttttt 1457

ttaaaaacat acataatgaa acgaaaaatg aggaaaataa gggaaagtcg gcgtataatt 1517

tgtcacaaat attttattga cagaggctta tgaacgttga tataatttaa attttatttg 1577

acaaaaatgg gcttctggtg tatactgaat atagtgaggt ggatgcaatg gcgaaaacgt 1637

tgtccgatat taaaagatcg cttgatggac atttgggaaa aaggctgacg ttaaaagcaa 1697

acggtggccg ccgaaaaacg attgagcgtt cgggcatttt agctgagacg taccсttctg 1757

tttttgtgat acaactagac caagacgaga attcgtttga aagagtttca tacagttatg 1817

cggatattct tactgagacg gttgaattga ggttttccga tgataaaacc agctcagtag 1877

ccctttaata agcagtggac 1897

<210> 133
<211> 299
<212> PRT
<213> Bacillus licheniformis

<400> 133

Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile Gly Asp Met Val Val
1 5 10 15

Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg Ile Ile Arg Ile Asp
20 25 30

Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu His Gly Asp Glu Val
35 40 45

Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu Glu Ile Val Arg Glu
50 55 60

Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu Thr Arg Met Lys Glu
65 70 75 80

Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu Leu His Asp Lys His
85 90 95

Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln Gln Gln Tyr Phe His
100 105 110

Met Pro Gly Arg Val Leu His Leu Asp Gly Asp Ser Ala Tyr Leu Lys
115 120 125

Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val Pro Val Tyr Gly Ile
130 135 140

His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile Glu Glu Leu Ile Asp
145 150 155 160

Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly His Asp Ala Tyr Ser
165 170 175

Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala Tyr Arg His Ser Lys
180 185 190

Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg Lys Ile Pro His Leu
195 200 205

Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln Ser His Phe Glu Ser
210 215 220

Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser Pro Ser Arg Val Asn
225 230 235 240

Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala Lys Ile Ser Phe Thr
245 250 255

Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val Leu Arg Asn Thr Leu
260 265 270

Thr Arg Glu Lys Gly Leu Gly Gly Ile Glu Thr Arg Gly Val Leu Arg
275 280 285

Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp
290 295

<210> 134
<211> 1010
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(734)

<400> 134
atcattaaag atatcgtgct ggggacgatg tcgaaaaaga atatggaaga aaagctggga 60

ttataaaaaa tcccggcttt tttgcttata ttgcccaaaa aatggtgaaa atgaaaacaa 120

gctggaggtg attcaacatg aaaaaagcga aaaggcgaac atttgaagaa cttgtctcgg 180

aaaataaaaa ggagctcatg accaaccagg agtttcttga tcggctggaa gataagcttg 240

aagagaaatt taagctgaag tgagttttta aaaatcgatt catgtttacg ctcctttttg 300

agaatcctaa tgctgaaaag gagggataga catgccgaga gaacacgaca aacagtctaa 360

atttgccccg agccatcttg ggacaaaacc ggtagaatat aagcgcaaca aaggaaaaaa 420

gatgcatgat aaatcaggag aaacaccgat cattatgcag acaaaaggcg agtaaagatg 480

aaaaggaggc agagacccga atg aca cat caa aaa cat cat ccg gat gac aga 533
Met Thr His Gln Lys His His Pro Asp Asp Arg
1 5 10

tca gac aac gta gaa aag ctt caa gac atg gtg cag aac aca atc gaa 581
Ser Asp Asn Val Glu Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu
15 20 25

aac att gag gag tct gaa gag cag ctg tct ttt gcc agc gag gcg gaa 629
Asn Ile Glu Glu Ser Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu
30 35 40

cag gaa cag atc cgc gaa aaa aat gaa cgc cga aat gaa agc att gag 677
Gln Glu Gln Ile Arg Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu
45 50 55

gcg atg cgc aat gaa atc cat gac gag gcg gaa gcc cgc aaa aac gga 725

Ala Met Arg Asn Glu Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly
60 65 70 75

tat cat caa taaaccaggg cgacctggtt tttttgcatg aagcccgtcc 774
Tyr His Gln

gtcgtgtttt tgcccattgt atatgctaga attggattaa atacatttgt ggaaaaggga 834

gtagagggga aatttgtacg tctcaaaaaa agaaatagaa gtccgctatg ccgaaacaga 894

cccaaaatgg ggtgtcgtct atcacgccaa ttatttgatt ttgggatggg aggtaagccc 954

ggacggcttt aattaaagaa ctcggctttt ctttatgccg aaatgggaga aagacg 1010

<210> 135
<211> 78
<212> PRT
<213> Bacillus licheniformis

<400> 135

Met Thr His Gln Lys His His Pro Asp Asp Arg Ser Asp Asn Val Glu
1 5 10 15

Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu Asn Ile Glu Glu Ser
20 25 30

Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu Gln Glu Gln Ile Arg
35 40 45

Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu Ala Met Arg Asn Glu
50 55 60

Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly Tyr His Gln
65 70 75

<210> 136
<211> 2407
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1907)

<400> 136
gcatactgta aaaggccggg tgaatgaaga gcttttgaaa tcggtcgtga tagatccaaa 60

tggcgaattt tatgtatgcg gtccgctttc atttatgaaa agcgtgattg aaggattgca 120

aaaccttggc gtttcgatgg aaaacatccg ctatgagagc tttgcttcat ctcttgatat 180

gcaaatagcg aactaacctc aagaaggcag ctgtcaaacc gacagctgcc tcagcgtgtc 240

gacaaaccct cgcatgcgtt gtcagtcctg cgcgtcggtg ctcacgaatt ccaacattcg 300

ctccgctccg atgctcggcc ttcctagact gcaagggttt tcaatcacgc tgaaagaagg 360

atgacaaaat cccaaaacta agagctgttt tgggattttg tcagcaatct aaggcagctg 420

tcaatccgac agctgccttt catcttttca aaacccggct catacaataa agagaagtcc 480

aaccgggggg gatttgagta ttg agc ata cgg gag caa aaa gag ctg cag cgg 533
Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg
1 5 10

gcg att gaa gaa att acg gaa atc gcg gaa gga ttc ggc ctt gat ttt 581
Ala Ile Glu Glu Ile Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe
15 20 25

tac ccg atg aga tat gag att tgt cct gct gaa att att tat aca ttc 629
Tyr Pro Met Arg Tyr Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe
30 35 40

ggt gca tac ggg atg ccg aca aga tac agc cat tgg agt ttc gga aag 677
Gly Ala Tyr Gly Met Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys
45 50 55

caa ttt cac aaa atg aag ctt cac tat gac ttt ggc ttg agc aaa ata 725
Gln Phe His Lys Met Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile
60 65 70 75

tat gag ctt gtc att aat tca gat ccg tgt tat gcg ttt ttg ctg gac 773
Tyr Glu Leu Val Ile Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp
80 85 90

agc aat tca ttg att caa aat aag ctg att gtc gca cac gtc ctt gct 821
Ser Asn Ser Leu Ile Gln Asn Lys Leu Ile Val Ala His Val Leu Ala
95 100 105

cat tgt gat ttc ttt aaa aat aac tgc cgt ttt caa aat acg aag cgc 869
His Cys Asp Phe Phe Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg
110 115 120

gat atg gtt gaa agc atg tcg gcg aca gca gag cgg att aaa cat tat 917
Asp Met Val Glu Ser Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr
125 130 135

gaa acg gta cac ggt tca aaa gaa gtc gaa gca ttt ctc gat gcg gtg 965
Glu Thr Val His Gly Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val
140 145 150 155

ctg gcg att gaa gaa cac att gac cct tcg ctc gtg agg ccg aag ctg 1013
Leu Ala Ile Glu Glu His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu
160 165 170

tcg tgg agc gta gat gat gaa gag gaa gaa gaa acc ggc gcg ccg gcc 1061
Ser Trp Ser Val Asp Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala
175 180 185

act cct tat gac gac ctc tgg gaa ctg gat cat aaa gga tcg aaa gag 1109
Thr Pro Tyr Asp Asp Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu
190 195 200

aag aag aaa agg acg aaa aaa aag ttt ccg ccg aaa ccg gaa aaa gac 1157
Lys Lys Lys Arg Thr Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp
205 210 215

att ctg ctg ttc ata gaa gag cat tcg cgg gag ctg gag cct tgg cag 1205
Ile Leu Leu Phe Ile Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln
220 225 230 235

cgc gat att tta acg atg atg aga gag gaa atg ctg tat ttc tgg ccg 1253
Arg Asp Ile Leu Thr Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro
240 245 250

cag ctt gaa acg aaa atc atg aat gaa ggc tgg gcg tcc tat tgg cat 1301
Gln Leu Glu Thr Lys Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His

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                255                           260                           265

cag cga atc atc cgt gag ctt gat ctg aca tca agt gaa gcg atc gaa      1349
Gln Arg Ile Ile Arg Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu
        270                     275                     280

ttc gcc aag ctg aac gcg gga gtg gtt cag ccg tcc aaa acg gga atc      1397
Phe Ala Lys Leu Asn Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile
    285                     290                     295

aat cct tat tat ctc gga ttg aaa ata ttt gag gac ata gag gag cgc      1445
Asn Pro Tyr Tyr Leu Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg
300                     305                     310                     315

tac aac aac ccg aca gaa gac atg aaa aag atg ggg gta gag ccg aac      1493
Tyr Asn Asn Pro Thr Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn
                320                     325                     330

tct ggg aga gaa aaa ata ttt gaa gtc agg gag atc gaa tca gac att      1541
Ser Gly Arg Glu Lys Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile
            335                     340                     345

tca ttt atc agg aac tat tta acg aag gat ctt gtg atg cgg gaa gac      1589
Ser Phe Ile Arg Asn Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp
        350                     355                     360

ctc tac ttg ttt caa aaa cag gga agg gat tat aaa atc gtc gac aag      1637
Leu Tyr Leu Phe Gln Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys
    365                     370                     375

gat tgg gag gct gtg cgc gat cag ctt gtc agc atg aga gtc aac gga      1685
Asp Trp Glu Ala Val Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly
380                     385                     390                     395

gga ttt cct tat ttg aca gtt gag gac gga gat tac tta aag aac aat      1733
Gly Phe Pro Tyr Leu Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn
                400                     405                     410

gaa tta tac atc aag cat tgg tat gaa ggg atc gaa ctc gat ttg aag      1781
Glu Leu Tyr Ile Lys His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys
            415                     420                     425

tat ctt gaa aaa gtt ctg cct tac ctc cac cag cta tgg gga aga agc      1829
Tyr Leu Glu Lys Val Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser
        430                     435                     440

gtg cat gtc gag acc gtg ctc gaa gat aaa ccc gtc atg ttt tcc tat      1877
Val His Val Glu Thr Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr
    445                     450                     455

gat gga aag gct gtc cac cgc aga tat tta taaaggctgc attttggcag        1927
Asp Gly Lys Ala Val His Arg Arg Tyr Leu
460                     465

cctttttct tttaaagcgc aacgatttca actcgtccgt cctttcaaaa gaaatgccaa      1987

attaatgcac gtttgcccag ttttacgact tcattataaa aatgtaaaat aaagtattta      2047

atgatatttc taaaattgta attttagctg ccggaaagcg taaaaatgta gtatttaagt      2107

tacctttgaa atgtaaatga aatattatct acccttaaaa acttttttg aaaacgaata       2167

attaaggaat ttgacatagt aagtcaagac tatacctgat ggaattccct ccttataata      2227

gaagcagagg aagggctgaa gcagccgttc tcaaaaaaat gaaactgcta attttcgcct      2287

ttgaaaatat aaaatattct gctattggga ggacaacatg aaaaaacaag taataacagc      2347
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agcatcagcg gttgttttag gatcgacttt gtttgcggga gccgcttccg cgcaaaccat 2407

<210> 137
<211> 469
<212> PRT
<213> Bacillus licheniformis

<400> 137

Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg Ala Ile Glu Glu Ile
1 5 10 15

Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe Tyr Pro Met Arg Tyr
20 25 30

Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe Gly Ala Tyr Gly Met
35 40 45

Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys Gln Phe His Lys Met
50 55 60

Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile Tyr Glu Leu Val Ile
65 70 75 80

Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp Ser Asn Ser Leu Ile
85 90 95

Gln Asn Lys Leu Ile Val Ala His Val Leu Ala His Cys Asp Phe Phe
100 105 110

Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg Asp Met Val Glu Ser
115 120 125

Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr Glu Thr Val His Gly
130 135 140

Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val Leu Ala Ile Glu Glu
145 150 155 160

His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu Ser Trp Ser Val Asp
165 170 175

Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala Thr Pro Tyr Asp Asp
180 185 190

Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu Lys Lys Lys Arg Thr
195 200 205

Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp Ile Leu Leu Phe Ile
210 215 220

Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln Arg Asp Ile Leu Thr
225 230 235 240

Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro Gln Leu Glu Thr Lys
245 250 255

Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His Gln Arg Ile Ile Arg
260 265 270

Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu Phe Ala Lys Leu Asn
275 280 285

Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile Asn Pro Tyr Tyr Leu
290 295 300

Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg Tyr Asn Asn Pro Thr
305 310 315 320

Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn Ser Gly Arg Glu Lys
325 330 335

Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile Ser Phe Ile Arg Asn
340 345 350

Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp Leu Tyr Leu Phe Gln
355 360 365

Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys Asp Trp Glu Ala Val
370 375 380

Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly Gly Phe Pro Tyr Leu
385 390 395 400

Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn Glu Leu Tyr Ile Lys
405 410 415

His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys Tyr Leu Glu Lys Val
420 425 430

Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser Val His Val Glu Thr
435 440 445

Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr Asp Gly Lys Ala Val
450 455 460

His Arg Arg Tyr Leu
465

<210> 138
<211> 1291
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(791)

<400> 138
ggaattgttg tcaacaatat gttttacagt tcggggcaaa ttccgctgac cccgtcgggt 60

gaaatggtga ctggagacat cacagaacag acgcaccagg ttttccgcaa tttaaaagcc 120

gtgctgaaag aagcgggcgc ctctctggag actgtcgtca aagcaaccgt gtttctggcg 180

gatatgaatc aattcacaga ggtgaatgaa gtttacggac agtacttcga tacccacaaa 240

ccggcgagat catgcgttga ggtggcgagg ctgccgaaag acgcgcttgt tgaaatagaa 300

gtcatcgcat tagtgaaata gaaagaactc ttaaaagatg gttttggtct caaaatcatc 360

ttttttgttt ggaaaatttg tcaattcagt gttttttat cccaatatta caaaaatatt 420

tttaattatg caggaaaaca aaaaaagccg ttgaatagtt acactaatgt ttttatattg 480

ggaaaaggtg gtgaactact gtg gaa gtt acc gac gta aga tta cgc cgc gtg 533
Val Glu Val Thr Asp Val Arg Leu Arg Arg Val
1 5 10

aat acc gat ggt cgc atg aga gcg att gca tcc atc acg ctg gat cac 581
Asn Thr Asp Gly Arg Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His
15 20 25

gaa ttt gta gtg cat gat att cgt gta att gat gga aac aat ggt ctt 629
Glu Phe Val Val His Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu
30 35 40

ttc gtt gcg atg cca agt aag cgt aca cct gat gga gaa ttt cgt gat 677
Phe Val Ala Met Pro Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp
45 50 55

atc gct cat cca atc aac tca agc acc cgc gga aaa att cag gac gcg 725
Ile Ala His Pro Ile Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala
60 65 70 75

gtg tta aat gaa tat cat cgt ttg ggt gac gtt gag gaa ata gaa tat 773
Val Leu Asn Glu Tyr His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr
80 85 90

gaa gaa att gga gct tct taaaaaagaa gggcttatgg ataagccctt 821
Glu Glu Ile Gly Ala Ser
95

tttgttttga aaaaaaatga tcttatcata ataaaatgac aatatatggt ttgtgtctgc 881

gtataacagt agcaggaagg taaagcatgc gaactcggat aacaaagcgc atgcagaagg 941

aatcaatccg tctccctgat cagttaatcc taaatatgct ctaacatcc aaaatatgct 1001

gtcttgattt cccgatttct cattttggct tgcttgaaat caactcatat ttaggatata 1061

tttttctatg gataataggg ataatggagg ccaatacatg gataagcggt ttgcagttgt 1121

gttagcagct ggtcaaggaa caagaatgaa atcaaagcta tataaagttc ttcatcctgt 1181

ttgcggaaaa cctatggtcg agcatgttgt cgatgaagct cgcaagctat cattagaaaa 1241

acttgtcaca atagttggac atggtgcgga agatgtcaaa aaacagctcg 1291

<210> 139
<211> 97

<212> PRT
<213> Bacillus licheniformis

<400> 139

Val Glu Val Thr Asp Val Arg Leu Arg Arg Val Asn Thr Asp Gly Arg
1 5 10 15

Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His Glu Phe Val Val His
20 25 30

Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu Phe Val Ala Met Pro
35 40 45

Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp Ile Ala His Pro Ile
50 55 60

Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala Val Leu Asn Glu Tyr
65 70 75 80

His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr Glu Glu Ile Gly Ala
85 90 95

Ser

<210> 140
<211> 1694
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1451)

<400> 140
gctcgagggg gatgcgcttt cgtcaaccct taaaaacgcc cgatatctgc cggaatggct 60

gaagctgcaa aaggaaatta aacaagagat tgaaaaagcg atcaaatcga atcagcgcga 120

aacgctgatt gatgccatca accaaaaaat taaaaaatac aacctcacct gtccgaacca 180

attccaaaaa ggccttgttt cagccaaaaa cctcgaaagt cagctcaaat attggagctg 240

atgccattcc ctgcacttat tcataaaaat aattgccaat aacaatcatc ttatgtaaaa 300

taaaggtaat atttatgctt ttaaaaagga gaaaggatga atgaagaagt ggaagcgaaa 360

gcggcatacg aaaaagcggc ctggctcctg aatcagtggt acaccatgat caagcgccat 420

gaagcgctcc aggctgtatc tttgaggtac gagatccaaa acctgctttc taaaatggag 480

aaaagcggag atctggagct ttg ttt tca gct gtt gga cta tcg ctg caa att 533
Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile
1 5 10

gat gat gga gca gtt tca gaa tca gcc gag ctt ttc cgg aaa att aaa 581
Asp Asp Gly Ala Val Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys
15 20 25

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agg cag aag gaa acg gtt aag agc gcg gat gac atc att cag tac tat      629
Arg Gln Lys Glu Thr Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr
        30                  35                  40

ttt ttc ttt ttt tca ggc atg tat gag ttt tat gag aaa aac tat ttt      677
Phe Phe Phe Phe Ser Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe
    45                  50                  55

gag gcg atc agc tgt tac aag aaa gcg gaa gcg aag ctg cat aaa ctg      725
Glu Ala Ile Ser Cys Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu
60                  65                  70                  75

acc gat gaa att gaa aaa gcg gaa ttt tat tat aaa atc gcg acc gcc      773
Thr Asp Glu Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala
                80                  85                  90

tac tac caa ata gac gat cat ttc aga tcg ttg aac tac tcc gaa aaa      821
Tyr Tyr Gln Ile Asp Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys
            95                  100                 105

gcg ctc tca ctt ttc agc aag cat aaa gaa tac ata gac aaa acg atc      869
Ala Leu Ser Leu Phe Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile
        110                 115                 120

gga tgc gaa atg ata ctc gga tcg gtg cag ttt gaa ttg ttc cgc atc      917
Gly Cys Glu Met Ile Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile
    125                 130                 135

aaa caa gct gag gag cac tac ggg cgg gcg ctt gat cag gcc gtt gcc      965
Lys Gln Ala Glu Glu His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala
140                 145                 150                 155

ctt caa aac cgg cga atc atc ggg ctg atc tat cat aat atg gga ctg      1013
Leu Gln Asn Arg Arg Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu
                160                 165                 170

aac tat gcc aaa tgc ggc atg ccg ctt ttg gcg gag gag cac ttt aga      1061
Asn Tyr Ala Lys Cys Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg
            175                 180                 185

aaa gcc ctt tca atc ggt gtc cat gag caa tcg gtt ttt ggc att aac      1109
Lys Ala Leu Ser Ile Gly Val His Glu Gln Ser Val Phe Gly Ile Asn
        190                 195                 200

acc ctt ttc gag ctg tct cac ctc atg tac aaa aac ggt tct ccc gaa      1157
Thr Leu Phe Glu Leu Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu
    205                 210                 215

gaa gcg aga cgt ctc tgc aaa gag gga ttt acc aga tcg gcc gaa tta      1205
Glu Ala Arg Arg Leu Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu
220                 225                 230                 235

gga gag gat gaa tac gca gcg aag ttc agg ctg att ttc gcc ctg tat      1253
Gly Glu Asp Glu Tyr Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr
                240                 245                 250

gac gct ggc cat ccg ctc gat att gaa ttt tcg ctt gaa tat atg agt      1301
Asp Ala Gly His Pro Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser
            255                 260                 265

gat aaa cgg cta tgg ccg cat gtt gct gaa ctg aca aaa gat att gcc      1349
Asp Lys Arg Leu Trp Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala
        270                 275                 280

gac tat tac atg aag tca ggc gac cat gaa aaa agc gcg ctt tac ctg      1397
Asp Tyr Tyr Met Lys Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu
    285                 290                 295
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gaa aaa tcg cag cat gcg aaa aat caa ata tat aaa atg aag gag ggg 1445
Glu Lys Ser Gln His Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly
300 305 310 315

att ata tgaaaaaaa catttgtttt ttcgccgtca tgcttgtttg cctgatgggg 1501
Ile Ile

ggaagcttca cagctgattc tgcagcacag gacggatcgt ttcagccatt gggaaagtcg 1561

gtgtttcctg ccagcggacg atagagataa cttgccgaga tagaaatggc ctcccgtctt 1621

ttgctatcat cgtctcacct gaaggcaatt gaagggagca gtagtgatgc cgataaaaga 1681

gatttcgcgc tgc 1694

<210> 141
<211> 317
<212> PRT
<213> Bacillus licheniformis

<400> 141

Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile Asp Asp Gly Ala Val
1 5 10 15

Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys Arg Gln Lys Glu Thr
20 25 30

Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr Phe Phe Phe Phe Ser
35 40 45

Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe Glu Ala Ile Ser Cys
50 55 60

Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu Thr Asp Glu Ile Glu
65 70 75 80

Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala Tyr Tyr Gln Ile Asp
85 90 95

Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys Ala Leu Ser Leu Phe
100 105 110

Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile Gly Cys Glu Met Ile
115 120 125

Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile Lys Gln Ala Glu Glu
130 135 140

His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala Leu Gln Asn Arg Arg
145 150 155 160

Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu Asn Tyr Ala Lys Cys
165 170 175

Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg Lys Ala Leu Ser Ile
180 185 190

Gly Val His Glu Gln Ser Val Phe Gly Ile Asn Thr Leu Phe Glu Leu
195 200 205

Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu Glu Ala Arg Arg Leu
210 215 220

Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu Gly Glu Asp Glu Tyr
225 230 235 240

Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr Asp Ala Gly His Pro
245 250 255

Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser Asp Lys Arg Leu Trp
260 265 270

Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala Asp Tyr Tyr Met Lys
275 280 285

Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu Glu Lys Ser Gln His
290 295 300

Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly Ile Ile
305 310 315

<210> 142
<211> 1260
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1244)

<400> 142
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cggccctcgg caccattgat cacacacatg ccggtgtggc ggaattggca gacgcgcacg 120

actcaaaatc gtgttccttc gggagtgtcg gttcgacccc gaccaccggt atcactaaac 180

atcgtattgc caaacgatga aagagcgttc ctacaaaagg agcgctcttt ttatttattc 240

cttatcttgg aacgaagccg taagaatttt ttcttaagga ctgcgagctc cggaagctac 300

gggaacatac cgtgagattt atcgaaatga gcttaatacg gtgcagaaac ttttacaaaa 360

gcaaaaatat atctgatgat ttattatcta tttatagggc gaaaagtaaa ttattgatac 420

aaacttcttt gcaaagattg gtaactttct gtaaaatgtt ctcatagcga tagaggcagt 480

aaagtgtggg aggtttgaca atg aaa gca gca gcc tct gtg aac gta gcc aat 533
Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn
1 5 10

ctc atc aat cag tgg tat gtt cac ata aaa aag aga gat gtt tca aat 581

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Leu Ile Asn Gln Trp Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn
            15                  20                  25

gcc gta gaa ctt agg gac aga ata aaa ggc ctt tta aac gta atg gaa      629
Ala Val Glu Leu Arg Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu
        30                  35                  40

gaa gat cag gat gtt ttg ctt tac ttt aat cta ctt gat tac agg ttc      677
Glu Asp Gln Asp Val Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe
    45                  50                  55

aga gta tta atg gaa gac gtc gcg ggg gag ccg cag ctt ccg cct att      725
Arg Val Leu Met Glu Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile
60                  65                  70                  75

gct gaa gat aag gcg aag aca gac ggt ttg tta cga tac tat tac ttt      773
Ala Glu Asp Lys Ala Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe
                80                  85                  90

ctc ttt aaa gga atg tat gaa agt gcg agg agc aac tac tct aaa gcg      821
Leu Phe Lys Gly Met Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala
            95                  100                 105

ctt aat tgt ttt aga gtt gcc gag cgg cag ctc gat aat gtc gaa gat      869
Leu Asn Cys Phe Arg Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp
        110                 115                 120

gaa atc gaa aag gcc gag ttt cat tat aag ctt gga aat ctc tat tat      917
Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr
    125                 130                 135

ttt acg aaa aca act cta ctt tct ttt cat cat ctt tca atc gcg aag      965
Phe Thr Lys Thr Thr Leu Leu Ser Phe His His Leu Ser Ile Ala Lys
140                 145                 150                 155

agc att tat agg gct tat gaa gaa tat aag aca cag tcg ata aac tgt      1013
Ser Ile Tyr Arg Ala Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys
                160                 165                 170

acg gtg ctg ctc gca ctc aat tat ata gac gac gga cgt tta aca aga      1061
Thr Val Leu Leu Ala Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg
            175                 180                 185

gct gaa aat atg ctt aag agt tgc gca gaa aga ctg atc aag atg ggc      1109
Ala Glu Asn Met Leu Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly
        190                 195                 200

gat aat cat ctg ctg gcg gct gtc tac tat gat ctc ggc ttt tta aaa      1157
Asp Asn His Leu Leu Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys
    205                 210                 215

att caa gag gat aaa cat gaa gaa gca ctc gag tat ttc gac ctc tca      1205
Ile Gln Glu Asp Lys His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser
220                 225                 230                 235

ttt aaa acg ggt gat atc gaa aaa aat gag ccg ggg act tagctcgata      1254
Phe Lys Thr Gly Asp Ile Glu Lys Asn Glu Pro Gly Thr
                240                 245

gatgta                                                              1260


&lt;210&gt;  143
&lt;211&gt;  248
&lt;212&gt;  PRT
&lt;213&gt;  Bacillus licheniformis

&lt;400&gt;  143
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Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn Leu Ile Asn Gln Trp
1   5   10   15

Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn Ala Val Glu Leu Arg
            20   25   30

Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu Glu Asp Gln Asp Val
        35   40   45

Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe Arg Val Leu Met Glu
    50   55   60

Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile Ala Glu Asp Lys Ala
65   70   75   80

Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe Leu Phe Lys Gly Met
                85   90   95

Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala Leu Asn Cys Phe Arg
            100   105   110

Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp Glu Ile Glu Lys Ala
        115   120   125

Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr Phe Thr Lys Thr Thr
    130   135   140

Leu Leu Ser Phe His His Leu Ser Ile Ala Lys Ser Ile Tyr Arg Ala
145   150   155   160

Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys Thr Val Leu Leu Ala
                165   170   175

Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg Ala Glu Asn Met Leu
            180   185   190

Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly Asp Asn His Leu Leu
        195   200   205

Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys Ile Gln Glu Asp Lys
    210   215   220

His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser Phe Lys Thr Gly Asp
225   230   235   240

Ile Glu Lys Asn Glu Pro Gly Thr
                245

<210> 144
<211> 2119
<212> DNA

<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1619)

<400> 144

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tacgcagtcg aaatgaaccg tcttatcaag ttcgagatgg aagggtctat tggttaaccc      60

ttgatactaa agggggtgat cagacttcga tttgattgca cccgaataaa ctttatgttt     120

gtgtaccgca gatataatct attgcctatc gattttctaa aaggcgtaga aatgtatctg     180

cggtttttttc tttagctttt tatttcataa aagaggtttg aattttgctt cctaacgatt    240

agttatgcca aattacatat caacaggaaa atataatcct tcatctgttc tgccttcctt     300

cctatacttc taaaattcac ccaaacacgg aaaacgaatc atattgatta ggccaaaaaa     360

cctctaactt ataaagattt ctgagaatgt tgttgtgaaa aattattact tttatgtaaa     420

atgatgacta tgaataaaaa gggaattgct attttgggtt tttagaaaaa ttataatctt     480

gcgagaaagg aagaggatat gtg agc gtg ata cca tat gat ttg gtt gcg acg     533
                      Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr
                      1               5                   10

aaa atg aat ttt tgg tat aca gcc tta aaa aac aat tgg aca ggc aag       581
Lys Met Asn Phe Trp Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys
            15                  20                  25

gct gag gat act aag aaa gaa gtt gaa cga gaa tta gaa caa atg gaa       629
Ala Glu Asp Thr Lys Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu
        30                  35                  40

caa aat cag gat gtg att gtc tat tac aac tta ctg ctc ttc cgg cat       677
Gln Asn Gln Asp Val Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His
    45                  50                  55

aat ctt caa ctt gat tat atg tat tct aaa ccc ggt gta aat tta aat       725
Asn Leu Gln Leu Asp Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn
60                  65                  70                  75

agt cgt ttt gat gag ttc aaa aag att cgc gat cag aat aat ctg gaa       773
Ser Arg Phe Asp Glu Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu
                80                  85                  90

gga atg ttg gat tat tat tat cat ttt ttc gct gga atg tat cat ttc       821
Gly Met Leu Asp Tyr Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe
            95                  100                 105

aga caa aaa gaa tta atc ctt gcg ctg aat ttt tat agg gat gcc gag       869
Arg Gln Lys Glu Leu Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu
        110                 115                 120

aaa aaa ctc gat tct ttt gat tgt gat gaa ctg gaa aag gct gaa ttt       917
Lys Lys Leu Asp Ser Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe
    125                 130                 135

tat ttc aag gca tct gaa gtg tat tac cat atg aaa caa acc atc ttt       965
Tyr Phe Lys Ala Ser Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe
140                 145                 150                 155

tcg atg aat tat gca agt cgt gcg tat aac tta ttc aaa aag tat gat      1013
Ser Met Asn Tyr Ala Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp
                160                 165                 170
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act tac ggt gag cgt cga gta caa agt cag ttt att att gca ggt aac      1061
Thr Tyr Gly Glu Arg Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn
            175                 180                 185

tgg cta gat cat atg tat ccc gaa aaa gct cta cat aat tta aat aaa      1109
Trp Leu Asp His Met Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys
        190                 195                 200

gag ctt aaa gag tca gag aca caa gga att ctt cat ctt atg ggt tca      1157
Glu Leu Lys Glu Ser Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser
    205                 210                 215

tca cat tta aat atc gga ata tgc tac aat aaa ttg gaa gat gtc gat      1205
Ser His Leu Asn Ile Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp
220                 225                 230                 235

aaa gca acc tac aat ttt caa aga gct ctg aac ctt tat aaa gag gag      1253
Lys Ala Thr Tyr Asn Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu
                240                 245                 250

aag cat agt ttt ttg cca aaa aca tta ttc aac ctc gca cat gtc agg      1301
Lys His Ser Phe Leu Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg
            255                 260                 265

gca aag caa ggg aag ttg tca ata act gat gac cta tac tat gaa ggc      1349
Ala Lys Gln Gly Lys Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly
        270                 275                 280

aaa gag ttg gct gaa aag aac aag aat tta gat atg ctt gca aag ttt      1397
Lys Glu Leu Ala Glu Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe
    285                 290                 295

gat tta ata aaa ggg ctt tat ctt tca ttt gat ctg gat atg gtt cgc      1445
Asp Leu Ile Lys Gly Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg
300                 305                 310                 315

gaa tcg ttc aag ttt ttc gaa agt aaa ggc aag tat gca gac atg gag      1493
Glu Ser Phe Lys Phe Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu
                320                 325                 330

gaa tac ggt ctt ata gcg gct gaa cta tta gag aaa aaa gaa aaa att      1541
Glu Tyr Gly Leu Ile Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile
            335                 340                 345

cga gat gca gtg gaa ttc tac cgg ata aca gtt aat gcg aga aga caa      1589
Arg Asp Ala Val Glu Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln
        350                 355                 360

att caa agg agt gct ttt cta cat gta aac taaatcgttc taggggtagt        1639
Ile Gln Arg Ser Ala Phe Leu His Val Asn
    365                 370

taaagcagca ggatttctta ctataaaaaa gaatttcccc cagcattatt aaaacctcaa    1699

attttgatta cttgattatt attttaagta atcgcagaaa gaaaggtcgg tctatggcaa    1759

gctatttaaa atccagaatc gtatcttatc tgtttattct tttggaagtg gggaccggat    1819

tcgcaatttg cgaggtgtca atggaaaatc cgaattactc ctcagcttgc gcggtcttta    1879

tcataggttt tacgattggg gaatgcttca tgattagaaa atggtaaatt ttgatcatga    1939

cgggatactc tttaccctct tctataaaag tgggacagac agttgaaaag ccggtaaatt    1999

catagccttg tatttcaaca gtaacttctt ctatatgcgg gtttcatttt ttcatctttg    2059

cttaatacat taaatcacct cctttataca gtatttgtcc attaaagaag aacaggatct    2119
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<210> 145
<211> 373
<212> PRT
<213> Bacillus licheniformis

<400> 145

Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr Lys Met Asn Phe Trp
1   5   10   15

Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys Ala Glu Asp Thr Lys
            20   25   30

Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu Gln Asn Gln Asp Val
        35   40   45

Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His Asn Leu Gln Leu Asp
    50   55   60

Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn Ser Arg Phe Asp Glu
65   70   75   80

Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu Gly Met Leu Asp Tyr
                85   90   95

Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe Arg Gln Lys Glu Leu
            100   105   110

Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu Lys Lys Leu Asp Ser
        115   120   125

Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe Tyr Phe Lys Ala Ser
    130   135   140

Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe Ser Met Asn Tyr Ala
145   150   155   160

Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp Thr Tyr Gly Glu Arg
                165   170   175

Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn Trp Leu Asp His Met
            180   185   190

Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys Glu Leu Lys Glu Ser
        195   200   205

Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser Ser His Leu Asn Ile
    210   215   220

Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp Lys Ala Thr Tyr Asn
225   230   235   240

```
Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu Lys His Ser Phe Leu
                245                 250                 255

Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg Ala Lys Gln Gly Lys
            260                 265                 270

Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly Lys Glu Leu Ala Glu
        275                 280                 285

Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe Asp Leu Ile Lys Gly
    290                 295                 300

Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg Glu Ser Phe Lys Phe
305                 310                 315                 320

Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu Glu Tyr Gly Leu Ile
                325                 330                 335

Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile Arg Asp Ala Val Glu
            340                 345                 350

Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln Ile Gln Arg Ser Ala
        355                 360                 365

Phe Leu His Val Asn
    370


&lt;210&gt;  146
&lt;211&gt;  1405
&lt;212&gt;  DNA
&lt;213&gt;  Bacillus licheniformis


&lt;220&gt;
&lt;221&gt;  CDS
&lt;222&gt;  (501)..(905)

&lt;400&gt;  146
tgtagggaaa gtgagttcat ggctcttatt agtgattgtc agctttctaa tcgtagccac      60

gttaaaacag gtgaagggga aagattccac tagagtggat gctggtcaat ttttataact     120

ctttatttta aaagggtttc gaggagctgt ggaagctgtt gcaggcatca ataaaagatc     180

aatattttct ttaagttgat cattcacaaa tcgaattact tctttattag gccaagtttc     240

attttcatgg atgcacaggg tttatccgca aattccttca aatagtaaac ccttcaagat     300

cgcggtggac gaaatttccc ttcgagaata ctgcaggtgc ggcttgaaaa agagcatata     360

gagattcagg cgtcttagca ggcgtctttt tgttgctgat tttattgcgg cataccgaaa     420

attttttcac ttttcaacct attatcaccc gaattatagt aatatattta caaaaatgaa     480

ataaaaaggt ataggcggaa gtg aaa cag tta ata ccc tcg tca aaa gtc gga     533
                      Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly
                      1               5                   10

gtg aaa atc cac gaa tgg tat aaa atg ata aga gag ttt agc gta ccg       581
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Val Lys Ile His Glu Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro
15 20 25

gat gca gag gct tta aaa gaa gaa gta gag aag gaa att aat caa atg 629
Asp Ala Glu Ala Leu Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met
30 35 40

gaa gaa gat cag gac tta ctc ctt tac tat cag ttg atg tgt ttt aga 677
Glu Glu Asp Gln Asp Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg
45 50 55

cat caa tta atg tta gaa tat tta gaa cct act aac aaa aga aaa caa 725
His Gln Leu Met Leu Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln
60 65 70 75

gga caa tca ata aac aaa ttg ttg gcc caa atc gag gag cct cga aga 773
Gly Gln Ser Ile Asn Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg
80 85 90

gat tta aat ggc ctc ctt agt tac tac tca ttt ttc ttt agg ggc atg 821
Asp Leu Asn Gly Leu Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met
95 100 105

tat gaa ttt gag aaa aaa cag tac atc aaa gca ata gag ttt tat cga 869
Tyr Glu Phe Glu Lys Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg
110 115 120

aac gca gaa aaa cag ttg gct ctc att acg atg tta tagaacaagc 915
Asn Ala Glu Lys Gln Leu Ala Leu Ile Thr Met Leu
125 130 135

cgagtttcac tttaaaatgg ctgaagcata ctacatcatg aaacagacac atgtatcata 975

tattaagggc ctttaaaata tacaataatc atgaactcta cacagtccgt aaaatccaat 1035

gtttatttgt tatcgcgggt aactatgacg atttaatgcg ccatgacaaa gccttacccc 1095

acctggaaaa tgcacttgaa ttagcgatag agatcgacaa taaaaggctc attagttctg 1155

cctattttaa tatagccgac tgtcatgaat gtatgggaga cattgatgca gcagttgaat 1215

atgctgaaaa agccgtagag attaatctaa aagaagaata taacaaccta ccacaatcat 1275

tatattactc tactcaactt ctttttaagc agaaaaacta cgagcgcgca atcgagatat 1335

ttcttattgg ttagacaaac agctcgaaaa ttcaacgata ccctattcac ttctctattt 1395

gaatatcttg 1405

<210> 147
<211> 135
<212> PRT
<213> Bacillus licheniformis

<400> 147

Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly Val Lys Ile His Glu
1 5 10 15

Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro Asp Ala Glu Ala Leu
20 25 30

Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met Glu Glu Asp Gln Asp
35 40 45

Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg His Gln Leu Met Leu
    50   55   60

Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln Gly Gln Ser Ile Asn
65   70   75   80

Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg Asp Leu Asn Gly Leu
                85   90   95

Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met Tyr Glu Phe Glu Lys
            100   105   110

Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg Asn Ala Glu Lys Gln
        115   120   125

Leu Ala Leu Ile Thr Met Leu
    130   135

<210> 148
<211> 2104
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1604)

<400> 148
ggaaacgtca gtccctgtcg gttctgtcca ggatacttta tagacgcctt cagtcagctt   60

gacgatatcg gctttttgat cgcgaaccca gcgtccccca accattccgc tgtgaatgcg   120

gtaatcgatg gtatggtcat ttttaatgta gatttcatat tcccatccgt tttcatacgt   180

atagatcata tggcttccta caaactcttt tacatcttga ttcatatgaa ccgctccttt   240

atttgtttat tgtaatcgaa acatgttgat atttacatat ataattataa aatgccgtca   300

aaaaagatgt caaacgaaaa tacttcctga gagatttgca caaataaaga agattgttac   360

gattaatgtc agaattttga gttatcttag gaaattatgc caatatttag aaaagtgatt   420

gtcaaaaaat aagcgattct gtaaatgaaa aaacaaccca taaaaaggaa atgacatggg   480

aagaaaggaa ggataaacga ttg aag aca aaa att gcg tat gag gaa gtt gcg   533
                     Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala
                     1   5   10

gga atg ctt aat caa tgg tat gtc atg atc aag cgt cac gaa gta tca   581
Gly Met Leu Asn Gln Trp Tyr Val Met Ile Lys Arg His Glu Val Ser
            15   20   25

caa gcg gtc tcg att aaa tgc gac att gag cac cag ctg ccg aat atg   629
Gln Ala Val Ser Ile Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met
        30   35   40

gaa gaa aat caa gat ctg ctt ctt tat ttt aat ctt tta gac tat cgg   677
Glu Glu Asn Gln Asp Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg
    45   50   55

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cac aag ctg ctg aca gaa gag ttt gcc gct tcc aac aaa ctg ttc gag      725
His Lys Leu Leu Thr Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu
60                  65                  70                  75

gat att cag gag caa aaa gcc gat atg caa agc aca gat gac atg att      773
Asp Ile Gln Glu Gln Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile
                80                  85                  90

gaa tat tat tat ttc ttt ttc gct ggc atg tac gaa ttt cat aag aag      821
Glu Tyr Tyr Tyr Phe Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys
            95                  100                 105

gat tat aca aat gca atc aat tat tat aaa tta gcc gag gaa aag ctc      869
Asp Tyr Thr Asn Ala Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu
        110                 115                 120

agg aca atc ccc gat caa atc gaa atc gcc gaa ttc cat tac aaa ctg      917
Arg Thr Ile Pro Asp Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu
    125                 130                 135

gct atc gcc tac tat caa atc aaa caa aat ttc ctt tcc tta aac cat      965
Ala Ile Ala Tyr Tyr Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His
140                 145                 150                 155

gcg aaa aca gct cta aaa acc ttc aaa gca cat gat gat tac att caa      1013
Ala Lys Thr Ala Leu Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln
                160                 165                 170

aaa gcg atc agc aac gat atg ctg atc ggg gca aat aaa ctc gat tta      1061
Lys Ala Ile Ser Asn Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu
            175                 180                 185

ttt cgt ttt gat gaa gcc gaa cag cat tac aag caa gcc ctt aaa gac      1109
Phe Arg Phe Asp Glu Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp
        190                 195                 200

gcg gca ctg atc aaa cat cat gtc ctc ctc ggc atg gct cac cac aac      1157
Ala Ala Leu Ile Lys His His Val Leu Leu Gly Met Ala His His Asn
    205                 210                 215

tta ggg ttg agc tat gtc aat cgc aac ctc ctc aca ttg gct gaa cat      1205
Leu Gly Leu Ser Tyr Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His
220                 225                 230                 235

cat ttc aaa gaa gcg ctg ctt atc aaa gag cat gaa gaa tcg gtt tac      1253
His Phe Lys Glu Ala Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr
                240                 245                 250

ggc atc cat tcc atg ttt gaa ctg aca cat gtg ctg tac aaa tca aat      1301
Gly Ile His Ser Met Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn
            255                 260                 265

gtt gtc aaa gaa gca cgc aaa ttg tat gaa aaa gga ttt ttc cgt gcg      1349
Val Val Lys Glu Ala Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala
        270                 275                 280

gaa aaa gca gga gaa agg gaa tat ttg tcg aaa ttt aaa ctt att cat      1397
Glu Lys Ala Gly Glu Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His
    285                 290                 295

gct ctg tat gat gaa cag gat cca ctt acg gtt gaa cat gct tta gaa      1445
Ala Leu Tyr Asp Glu Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu
300                 305                 310                 315

tat ctt aaa acg atc aat ctc tgg acg gat gta gcg gaa tta aca ttt      1493
Tyr Leu Lys Thr Ile Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe
                320                 325                 330
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gat atc gca ctt tac tat aaa gaa aat gga gat gca gac aaa gct gcc 1541
Asp Ile Ala Leu Tyr Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala
335 340 345

gaa tat ttt gaa gaa tct cat cat gca aga gac caa att ctt aaa aga 1589
Glu Tyr Phe Glu Glu Ser His His Ala Arg Asp Gln Ile Leu Lys Arg
350 355 360

acg gag gag tta aag tgaaaaagat gattgccgtt gcgttgactg ccgtctttgc 1644
Thr Glu Glu Leu Lys
365

aagccttgtc gttttaagtt tttcgtctca gccgaaggga gatgccgagt ttgccggccg 1704

agccattttt cttgacgata agccggctca gctgatggcg ggcagagcga tctttctcga 1764

cagctttgac ggaaattcgc cagccgcctg acaaaacacc gcataaccct gcttgtcacc 1824

ggacaagctc tcttcgaaaa gcgccgccag cggcgctttt tttatgaaag caaatataac 1884

cggcgtccct gcaaatcgct tgcgaagatt aaaaatatga aacacatgac aggaatggcg 1944

ctcaccggct tttggtcgaa tcctattgaa aaatctgccc gatttatagt gcttgtcatt 2004

ctataaatcc ttataatggt cttaacgcca atgtgaggca tgccaataga cagattgcag 2064

gggaaattct atactgaaca gcgcaattta gcatgtaatc 2104

<210> 149
<211> 368
<212> PRT
<213> Bacillus licheniformis

<400> 149

Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala Gly Met Leu Asn Gln
1 5 10 15

Trp Tyr Val Met Ile Lys Arg His Glu Val Ser Gln Ala Val Ser Ile
20 25 30

Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met Glu Glu Asn Gln Asp
35 40 45

Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg His Lys Leu Leu Thr
50 55 60

Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu Asp Ile Gln Glu Gln
65 70 75 80

Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile Glu Tyr Tyr Tyr Phe
85 90 95

Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys Asp Tyr Thr Asn Ala
100 105 110

Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu Arg Thr Ile Pro Asp
115 120 125

Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu Ala Ile Ala Tyr Tyr
130 135 140

Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His Ala Lys Thr Ala Leu
145 150 155 160

Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln Lys Ala Ile Ser Asn
165 170 175

Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu Phe Arg Phe Asp Glu
180 185 190

Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp Ala Ala Leu Ile Lys
195 200 205

His His Val Leu Leu Gly Met Ala His His Asn Leu Gly Leu Ser Tyr
210 215 220

Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His His Phe Lys Glu Ala
225 230 235 240

Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr Gly Ile His Ser Met
245 250 255

Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn Val Val Lys Glu Ala
260 265 270

Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala Glu Lys Ala Gly Glu
275 280 285

Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His Ala Leu Tyr Asp Glu
290 295 300

Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu Tyr Leu Lys Thr Ile
305 310 315 320

Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe Asp Ile Ala Leu Tyr
325 330 335

Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala Glu Tyr Phe Glu Glu
340 345 350

Ser His His Ala Arg Asp Gln Ile Leu Lys Arg Thr Glu Glu Leu Lys
355 360 365

<210> 150
<211> 1381
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS

<222> (501)..(881)

<400> 150
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cagaggcttt aaaagaagaa gtagagaagg aaattaatca aatggaagaa gatcaggact 180

tactccttta ctatcagttg atgtgtttta gacatcaatt aatgttagaa tatttagaac 240

ctactaacaa aagaaaacaa ggacaatcaa taaacaaatt gttggcccaa atcgaggagc 300

ctcgaagaga tttaaatggc ctccttagtt actactcatt tttctttagg ggcatgtatg 360

aatttgagaa aaaacagtac atcaaagcaa tagagtttta tcgaaacgca gaaaaacagt 420

tggctctcat tacgatgtta tagaacaagc cgagtttcac tttaaaatgg ctgaagcata 480

ctacatcatg aaacagacac atg tat cat ata tta agg gcc ttt aaa ata tac 533
Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr
1 5 10

aat aat cat gaa ctc tac aca gtc cgt aaa atc caa tgt tta ttt gtt 581
Asn Asn His Glu Leu Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val
15 20 25

atc gcg ggt aac tat gac gat tta atg cgc cat gac aaa gcc tta ccc 629
Ile Ala Gly Asn Tyr Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro
30 35 40

cac ctg gaa aat gca ctt gaa tta gcg ata gag atc gac aat aaa agg 677
His Leu Glu Asn Ala Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg
45 50 55

ctc att agt tct gcc tat ttt aat ata gcc gac tgt cat gaa tgt atg 725
Leu Ile Ser Ser Ala Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met
60 65 70 75

gga gac att gat gca gca gtt gaa tat gct gaa aaa gcc gta gag att 773
Gly Asp Ile Asp Ala Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile
80 85 90

aat cta aaa gaa gaa tat aac aac cta cca caa tca tta tat tac tct 821
Asn Leu Lys Glu Glu Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser
95 100 105

act caa ctt ctt ttt aag cag aaa aac tac gag cgc gca atc gag ata 869
Thr Gln Leu Leu Phe Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile
110 115 120

ttt ctt att ggt tagacaaaca gctcgaaaat tcaacgatac cctattcact 921
Phe Leu Ile Gly
125

tctctatttg aatatcttga ggcgttatat atctattctg tgaataaaga agagatttta 981

gaggtattta aatacttgga ggagaataaa atatttgcat acatagaaga gctttcgctt 1041

gaagtctcta accaatacct tgaaagaaaa gaccatagaa actcaatcga gttccttcaa 1101

aaaatgatgt atgggcaaac aaaaattaaa aaaggggagt gtctctatga gtattaaaaa 1161

gctcgttatt cccattttag ccgccgcgtt attaacgatg ggtattagcg ttgtttcagc 1221

aaccgaccag tctgacggcg tatatcaaat cgctacccgt aagcaaacgt aagaaacgcc 1281

ccaaatgtgg ggcgcttttt atttctacgg tttcttaacg ttaaacatcg tgattaactt 1341

cttatcagct gtcggtaaga ttaacgtata ccattccgac 1381

<210> 151
<211> 127
<212> PRT
<213> Bacillus licheniformis

<400> 151

Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr Asn Asn His Glu Leu
1 5 10 15

Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val Ile Ala Gly Asn Tyr
20 25 30

Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro His Leu Glu Asn Ala
35 40 45

Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg Leu Ile Ser Ser Ala
50 55 60

Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met Gly Asp Ile Asp Ala
65 70 75 80

Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile Asn Leu Lys Glu Glu
85 90 95

Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser Thr Gln Leu Leu Phe
100 105 110

Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile Phe Leu Ile Gly
115 120 125

<210> 152
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<212> DNA
<213> Bacillus licheniformis

<220>
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<222> (501)..(1235)

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ccaaagaatt gatttggagc gggaaaaaat tgacgggggc cgaagcgcac gagcttcgga 120
tcgcagacgc cgtattcagc ggggactccg gccgttttgc gcgcatctat cttgaaaagc 180
ttctgcacgc tccgctggca gcgatgattg agacaaaaaa gatctatcag gcgttgaatg 240
gaggcaggct gcagaaaacg cttgaactcg agaaaacggc ccagatgaaa atgaggctga 300
caagcgacca tcaggaaggg atccgcgcat ttttagaaaa gcgccagccg caatttaacc 360
gtcagcaagt ataacaagag cggtccggca ggaaattgac cttgggaaat gatgtgcaga 420

aacaattgta aaaaaattta agtttccata aaatgattca taagatacag atctgtacga 480

agtcttggga ggcggcgaaa ttg aaa cag aag att cca tct gaa tac gtt gct 533
Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala
1 5 10

aga aag ctg aat gat tgg tac aac gcc att cgg aaa aat cag atc gcc 581
Arg Lys Leu Asn Asp Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala
15 20 25

gcc agt gaa tca ttg aaa gcg gaa att tta aat gat ttt caa gac atg 629
Ala Ser Glu Ser Leu Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met
30 35 40

gaa gaa aat cgg gac gtc ctg ctc tac tat tcg ctg ctt gaa ttc agg 677
Glu Glu Asn Arg Asp Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg
45 50 55

cat aaa ctg atg ctc agc tat ttg aaa ccg aaa gag act gaa aat att 725
His Lys Leu Met Leu Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile
60 65 70 75

gaa aaa aac ctc cgc gac tta gaa gaa aaa gaa gac caa atg acg ggt 773
Glu Lys Asn Leu Arg Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly
80 85 90

tta tta aac tat tat tac tgg ttt ttt aaa ggg atg tat gag ttc aaa 821
Leu Leu Asn Tyr Tyr Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys
95 100 105

caa aag cgg ttc gtc aaa gca atc ggc tgc tat aaa acg gct gaa caa 869
Gln Lys Arg Phe Val Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln
110 115 120

aaa gtc agc gca ctg gaa gac gag gtt gaa aaa gcg gaa ttt tat tat 917
Lys Val Ser Ala Leu Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr
125 130 135

aag ctt gcg gaa atc tac tat tat atc aac cag aga tac ctg tcg atc 965
Lys Leu Ala Glu Ile Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile
140 145 150 155

aac tat gcg acg cta gct tcc gac att ttt aac cgg tat gaa acg cta 1013
Asn Tyr Ala Thr Leu Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu
160 165 170

aaa gaa aaa aag att ttc tgc gat ttt atc att gcc ggt aat tgg gtt 1061
Lys Glu Lys Lys Ile Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val
175 180 185

gaa tcg atg aca tac gga ccc gcg ctg aaa agc ctg gcc aat gcg ctt 1109
Glu Ser Met Thr Tyr Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu
190 195 200

gaa gac gcc agg aaa atc aaa aac agc cat ttg acg gca gcc gct cat 1157
Glu Asp Ala Arg Lys Ile Lys Asn Ser His Leu Thr Ala Ala Ala His
205 210 215

ttt aat ttg gga aat tgc tat ttc cac caa gaa tcg tac cgg gaa gcc 1205
Phe Asn Leu Gly Asn Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala
220 225 230 235

tca gat cat atg gag cgc cct ttc cat ttt tgaacaggaa agttcatcat 1255
Ser Asp His Met Glu Arg Pro Phe His Phe
240 245

atattcccaa agtgctgtac aacttgatgt acgtccgtct caagcagggg aaccatgccg 1315

gagctgccgc ctgttatgaa aaaggcatcc gaagcgcggc atcgctcggg gatgaagaac 1375
acgcggcaaa gcttaacatt ctgtgcgggc tgtatttaga cggaggggat cagaaagccg 1435
tggaaaacgg atttgattat ttggagtcaa atcatttata tgctgctgtt gaagagctgg 1495
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aaactgttgt tcgtcgcggt gtcgctggct gttgtgttaa cgtcttcaag ctttttggca 1675
gatgcgggga aagcccccttc cttgtatgcg gacaaaatga tcacgactga caaggaggct 1735

<210> 153
<211> 245
<212> PRT
<213> Bacillus licheniformis

<400> 153

Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala Arg Lys Leu Asn Asp
1 5 10 15

Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala Ala Ser Glu Ser Leu
20 25 30

Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met Glu Glu Asn Arg Asp
35 40 45

Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg His Lys Leu Met Leu
50 55 60

Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile Glu Lys Asn Leu Arg
65 70 75 80

Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly Leu Leu Asn Tyr Tyr
85 90 95

Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys Gln Lys Arg Phe Val
100 105 110

Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln Lys Val Ser Ala Leu
115 120 125

Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr Lys Leu Ala Glu Ile
130 135 140

Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile Asn Tyr Ala Thr Leu
145 150 155 160

Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu Lys Glu Lys Lys Ile
165 170 175

Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val Glu Ser Met Thr Tyr
180 185 190

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Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu Glu Asp Ala Arg Lys
        195                 200                 205

Ile Lys Asn Ser His Leu Thr Ala Ala Ala His Phe Asn Leu Gly Asn
    210                 215                 220

Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala Ser Asp His Met Glu
225                 230                 235                 240

Arg Pro Phe His Phe
                245


<210>  154
<211>  2116
<212>  DNA
<213>  Bacillus licheniformis


<220>
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<222>  (501)..(1616)

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gttccagcgt ttgatctatt gcattgtgca gcgcctgaac atcaagagtc ttcatggcat     180

tctcctctaa tccttttcat tacaatcagt atatagttta ccactttata gaaagtactt     240

ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatttctat     300

tgattcattt cgattaccgt aaacaagttt gttgtagcat tctttaggct ctgtgactaa     360

accaaaaagc catttgtttt aaattggtct ttcggtatca cgaaaatttc gtttttttggg    420

ctgatagaag ttttgcaatt atgaattgta tgttaatctt taacataaaa aggatgttag     480

ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc     533
                      Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile
                      1               5                   10

aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa       581
Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu
            15                  20                  25

gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa       629
Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu
        30                  35                  40

gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat       677
Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His
    45                  50                  55

gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa       725
Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys
60                  65                  70                  75

tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc       773
Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly
                80                  85                  90
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ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct        821
Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser
            95                  100                 105

cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa        869
Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys
        110                 115                 120

aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat        917
Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr
    125                 130                 135

aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg        965
Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met
140                 145                 150                 155

tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat       1013
Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr
                160                 165                 170

gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att       1061
Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile
            175                 180                 185

gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag       1109
Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys
        190                 195                 200

gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt       1157
Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu
    205                 210                 215

tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct       1205
Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala
220                 225                 230                 235

att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca       1253
Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala
                240                 245                 250

aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga       1301
Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg
            255                 260                 265

aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa       1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu
        270                 275                 280

agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt       1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val
    285                 290                 295

tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa       1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu
300                 305                 310                 315

aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa       1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu
                320                 325                 330

ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat       1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn
            335                 340                 345

gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc       1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile
        350                 355                 360
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aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga        1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile
    365                 370

cccttgcttt gggcttgttg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac   1696

aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcaggtcat   1756

gtgatggcct gcctttttgg tgaaagaatt attttagttt gaaaaccaga acgattgtgt   1816

taatactcat ctttcttcgt cccttgtgtt ggaattttca tcatatcaat atttgaatat   1876

gcggctgtcc gcattattaa caattttaaa ttttttgcac aaattttata caaaggcaga   1936

caaaaacctt gatatatcaa tggttctatg ggtattttca accacgacca ccgatatcgc   1996

taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt   2056

ttattcctca tcaaagcgga gagccgccaa cataaacgca atgaccaact gttgtccgca   2116


&lt;210&gt;  155
&lt;211&gt;  372
&lt;212&gt;  PRT
&lt;213&gt;  Bacillus licheniformis

&lt;400&gt;  155

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp
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Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
            20                  25                  30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
        35                  40                  45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
    50                  55                  60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
65                  70                  75                  80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
                85                  90                  95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
            100                 105                 110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
        115                 120                 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
    130                 135                 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
145                 150                 155                 160
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Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
355 360 365

Leu Tyr Glu Ile
370

<210> 156
<211> 1576
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1268)

<400> 156

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caagcttcac aaaaccggtc gatgccggag aaatcgaaga aaagctggac acttcacacg     180
gcatgattcg gactgaggtg agaagcaagt ctgccgattc ccatcttgga cacgtgtttc     240
cggacggacc cggaccggac ggcctgcgct attgcatcaa ttcagccgcc ctccggtttg     300
tgccgaagga cgaccttgag aaagaaggat acggcgaata tgtcaaactg tttgaacgca     360
agaaatccgg agaggaaagc tgaggagagc agcatgcaag atgatccttt tttcaaaggg     420
tcatcttttt ttagaggatt ttctgctctg aaagcgaaaa aacattacaa tagatcatct     480
tgagaaaaga ggcagccgtt gtg aca tcc att tca aac aca gaa gac cgt tat     533
                      Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr
                      1               5                   10

tta atg ctg aca tgc agc aaa aaa att gaa tcc cat tat cat ata tac       581
Leu Met Leu Thr Cys Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr
            15                  20                  25

aca gat gag gag atc ccg cag atg ttt tcc tct cat ttt ctg cag ctg       629
Thr Asp Glu Glu Ile Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu
        30                  35                  40

cag gac gat ttt ccg ctg aca gag ctg tac tcc ctg ctc gtt cgg aca       677
Gln Asp Asp Phe Pro Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr
    45                  50                  55

ccc gaa att tta aaa cga aat tat gtt cat gtg aaa agc tct tat aag       725
Pro Glu Ile Leu Lys Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys
60                  65                  70                  75

cgg gat ctg cct ttt acg atg aaa aag tcg ctc ttt gat ctt ggc tat       773
Arg Asp Leu Pro Phe Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr
                80                  85                  90

att ctt gat gaa gaa ttg ttt tat tcc atc agg ctt gca gat tgg aaa       821
Ile Leu Asp Glu Glu Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys
            95                  100                 105

gga gat tcc cct ggt gta cgg gca gag tgg ggg acg gag aaa tcg ctc       869
Gly Asp Ser Pro Gly Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu
        110                 115                 120

att gac ggc tgc cgc atg atg cag gct tat gat aca ttg tct atc aat       917
Ile Asp Gly Cys Arg Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn
    125                 130                 135

gaa gcg ttt gcg aag gaa aag ctg ctg cgc aag tat cct ttt tat gag       965
Glu Ala Phe Ala Lys Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu
140                 145                 150                 155

gaa ggc atc att cag ctg tgt gtc tgc tac tcg gaa gaa ggc gaa ccg      1013
Glu Gly Ile Ile Gln Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro
                160                 165                 170

att gga tgt gct gag ctt tat ctc gat cac gac gaa aac gtt gct aaa      1061
Ile Gly Cys Ala Glu Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys
            175                 180                 185

atc gaa gaa gtc gcc att ttg gag cca tac cag cgg aaa ggc tat gga      1109
Ile Glu Glu Val Ala Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly
        190                 195                 200
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tcg ggc ctt atc aag cag atg ctc acc gcc gcc aaa caa tcg ggc atg 1157
Ser Gly Leu Ile Lys Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met
205 210 215

gaa tcg tgc tat ctt gta act tcg gga agc gat cag gtg aaa acg ttt 1205
Glu Ser Cys Tyr Leu Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe
220 225 230 235

tat gaa aag ctg ggc ttt cag cag aag gaa aag ctc acg aca ata ttt 1253
Tyr Glu Lys Leu Gly Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe
240 245 250

aaa tat ttg ttc gta taaagtaggc aggtgcacat accaattggg acttggcctg 1308
Lys Tyr Leu Phe Val
255

cataggctgg ggtgtagact ttatacgaaa ggatgataag cctgtgcatt actcccatta 1368

ttgctgtcct actggaggat acggctacgg gtttcacgga agaacacatt tgactcatcg 1428

ttgtcctctt tattttgctc atcattgtcg gtgcggcttt catttgctag ctaaaagccc 1488

gacgcccggc gcttgacatg ctcacaaagc cttcctccgg aaggtttttt ttggtttttg 1548

ttggaaaatt ttgcattcgt atgtaata 1576

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<211> 256
<212> PRT
<213> Bacillus licheniformis

<400> 157

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20 25 30

Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu Gln Asp Asp Phe Pro
35 40 45

Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr Pro Glu Ile Leu Lys
50 55 60

Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys Arg Asp Leu Pro Phe
65 70 75 80

Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr Ile Leu Asp Glu Glu
85 90 95

Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys Gly Asp Ser Pro Gly
100 105 110

Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu Ile Asp Gly Cys Arg
115 120 125

Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn Glu Ala Phe Ala Lys
130 135 140

Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu Glu Gly Ile Ile Gln
145 150 155 160

Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro Ile Gly Cys Ala Glu
165 170 175

Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys Ile Glu Glu Val Ala
180 185 190

Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly Ser Gly Leu Ile Lys
195 200 205

Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met Glu Ser Cys Tyr Leu
210 215 220

Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe Tyr Glu Lys Leu Gly
225 230 235 240

Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe Lys Tyr Leu Phe Val
245 250 255

<210> 158
<211> 1783
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1283)

<400> 158
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ttattgacaa acgcaaacga ttttttcgt cccggcccgc agtaagactg gcagccgatt 180

tccacttttg catccggatc aatttctttc agacggggca aaagcgtctt taaattggtg 240

gcctggcaat cgtcgcatac tcgaaattca ttagccattt catacgcttc ctttcgtttt 300

gttcatctgt ctttatgaaa ggcattcaac tgtgccgaac ttttataaaa aatgacacca 360

tccttcattt tacaaggatt ctttcattcc tgcaaggatc gcgctaaaaa aatcagttcc 420

tattctttta gcaaacttgt ataaatattt tccaaaatgg acaatctaat accaatactg 480

acaatgggag ttgagaagtg atg aaa caa aga caa gac gct tgg tct gag gaa 533
Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu
1 5 10

aat gat tta ctg ctt gct gaa acg gta ttg cgg cat gtc agg gaa ggg 581
Asn Asp Leu Leu Leu Ala Glu Thr Val Leu Arg His Val Arg Glu Gly
15 20 25

agc aca cag ctg aac gcc ttc gag gaa gtc gga gac aga ctg aac agg 629
Ser Thr Gln Leu Asn Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg
30 35 40

aca tca gcc gcc tgc ggt ttt aga tgg aac gca gtt gtc cgc cac caa 677
Thr Ser Ala Ala Cys Gly Phe Arg Trp Asn Ala Val Val Arg His Gln
45 50 55

tac gaa aaa gca ttg cag ctg gct aaa aaa cag agg aag caa aga atg 725
Tyr Glu Lys Ala Leu Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met
60 65 70 75

cgc gcc ctc gga aac gga cag ccg gcg aaa aaa cgc tta tta tac aag 773
Arg Ala Leu Gly Asn Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys
80 85 90

ccg ccg gtc gaa acg aat gct gaa cct cct gca gaa agc gtt gtt gag 821
Pro Pro Val Glu Thr Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu
95 100 105

cag aag aaa gca acc gca gat tca agc gaa cag cag ccg atc gcc agc 869
Gln Lys Lys Ala Thr Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser
110 115 120

gag cat ctg cct tat gtt gat gag agc ttt aaa gaa gag tta gct agt 917
Glu His Leu Pro Tyr Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser
125 130 135

tta tct cac ctt cta tcg cca aat cag ccg cag gcc ggc cat aca gcc 965
Leu Ser His Leu Leu Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala
140 145 150 155

gat aca tcg aaa gac atg acg atc gat gat gtg atc cgc ttc ctg caa 1013
Asp Thr Ser Lys Asp Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln
160 165 170

aac tat aca gga aac gaa gaa caa act gcc gct tta aaa atg gaa aat 1061
Asn Tyr Thr Gly Asn Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn
175 180 185

gaa cgt tta aaa cag gaa aac gaa gaa ctg acg aag aaa gtt gaa aag 1109
Glu Arg Leu Lys Gln Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys
190 195 200

ctt gaa gcg gaa gtc aaa aag ctg gaa aaa gac cag aca acc atc cag 1157
Leu Glu Ala Glu Val Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln
205 210 215

gaa gac tac gaa acg ctc gta aaa att atg aac cgt gca aga aaa cta 1205
Glu Asp Tyr Glu Thr Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu
220 225 230 235

gtt tta ttc gaa gaa gac gaa cac gct gcg ccc gcc ttc aaa atg gac 1253
Val Leu Phe Glu Glu Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp
240 245 250

cgg aac ggc aat tta gaa aaa atg gct gaa tagcgctctc agaggatgcg 1303
Arg Asn Gly Asn Leu Glu Lys Met Ala Glu
255 260

gcagagacgt tcaggcagca aggactgaca atgcatacaa acatttttcg atacgaggat 1363

accccttct ttaaaaaagg gggtattttt acctttctgc ggcttgcttt tatatgacaa 1423

aaatttcata atagggatag caattcataa ggcggggtat tcgatgaagt ttgttttata 1483

tgcggttcag ttcggcactg cggccctttt gtttttgttt tctgcattgg caagctggta 1543

tcaaggcagc gagcttttaa aggtgccgtg ggagtggaaa tatacagcca agtttacaag 1603

ttggctgtac ggagaggact ccattaaaaa cgcacataat atttcacagc ttgatttttt 1663

cgtctatgcg gccaagcata cgccggcaac cgttatttta atggccgtca gtttggcgta 1723

tatcatcgct ttggcggctt atcttctcat caaaacatat gtaaaacgaa aaagcgcttc 1783

<210> 159
<211> 261
<212> PRT
<213> Bacillus licheniformis

<400> 159

Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu Asn Asp Leu Leu Leu
1 5 10 15

Ala Glu Thr Val Leu Arg His Val Arg Glu Gly Ser Thr Gln Leu Asn
20 25 30

Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg Thr Ser Ala Ala Cys
35 40 45

Gly Phe Arg Trp Asn Ala Val Val Arg His Gln Tyr Glu Lys Ala Leu
50 55 60

Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met Arg Ala Leu Gly Asn
65 70 75 80

Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys Pro Pro Val Glu Thr
85 90 95

Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu Gln Lys Lys Ala Thr
100 105 110

Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser Glu His Leu Pro Tyr
115 120 125

Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser Leu Ser His Leu Leu
130 135 140

Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala Asp Thr Ser Lys Asp
145 150 155 160

Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln Asn Tyr Thr Gly Asn
165 170 175

Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn Glu Arg Leu Lys Gln
180 185 190

Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys Leu Glu Ala Glu Val
195 200 205

Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln Glu Asp Tyr Glu Thr
210 215 220

Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu Val Leu Phe Glu Glu
225 230 235 240

Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp Arg Asn Gly Asn Leu
245 250 255

Glu Lys Met Ala Glu
260

<210> 160
<211> 2311
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1811)

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tgagcagctc cagtactttc agttcattct gcttttgata aaacgtctga aacacaatga 120

ctttgtattg gtgtttcagc gcttcagcgg acatatgctt cataagctga gcgaagaagg 180

ggtggtccgc gtgtgggaca gacactgcga gaaacatcgt tttgttggat ctgagctttc 240

gtgcagacgt gttcgggatg tagtccaatt tttcgatgac ttccaaaacc cgcttccttt 300

tttcttcaga tacataggga tgatcgttca gtactcttga aacagttgtt tttgacacat 360

tacttaattt tgcaatttcg tcaatcgtag gcataaagtc acttcctgaa aaaaagagtt 420

gttatggtat cgattccatc atttaagata tgtcatgaaa tatgacaatt tcccaaaata 480

ataaaaatgg ggtgaaattg atg aaa acc gca aac gaa aac atg act tgc acg 533
Met Lys Thr Ala Asn Glu Asn Met Thr Cys Thr
1 5 10

agc aaa cag cta ttt gtc ctt ctg aat gat ttg aag gaa gga aag ctc 581
Ser Lys Gln Leu Phe Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu
15 20 25

gct ggt gaa tgc cgt ata gac gac aca ctg gcc aat caa aaa tta aaa 629
Ala Gly Glu Cys Arg Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys
30 35 40

gag aca ttg cag cag gat caa ttc gac ata acc gcc aat ttg ctg aac 677
Glu Thr Leu Gln Gln Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn
45 50 55

aga atg gat tcc ccg ccc tcc aga gtt gac ttt atg ccg ctt cat cga 725
Arg Met Asp Ser Pro Pro Ser Arg Val Asp Phe Met Pro Leu His Arg
60 65 70 75

ctg atc aca gaa gaa gaa gta gat gac gtg gtt cat gcg gtg aaa gac 773
Leu Ile Thr Glu Glu Glu Val Asp Asp Val Val His Ala Val Lys Asp
80 85 90

gtg ctg ccg acc ggg caa ttt aca agc ggt ttt tat gtt ggc gta ttt 821
Val Leu Pro Thr Gly Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe
95 100 105

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gaa gct gaa ata gct gct ttt ttg agc aaa aag cat gtc atg gct tca      869
Glu Ala Glu Ile Ala Ala Phe Leu Ser Lys Lys His Val Met Ala Ser
        110                 115                 120

tcc agc gga acc gat gcc atg att gtc gcg ctg aag gct gcg ggt gtt      917
Ser Ser Gly Thr Asp Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val
    125                 130                 135

gga caa ggt gat gaa gtc att atg cct gca aac agc ttt gct gca acg      965
Gly Gln Gly Asp Glu Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr
140                 145                 150                 155

gaa aac gcc gtg ctc gca gct gga ggc act ccg att ttc tgc gat att     1013
Glu Asn Ala Val Leu Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile
                160                 165                 170

gac cct gtt aca ttt tgc atg gat cct tca gaa att gaa gca tgt gtc     1061
Asp Pro Val Thr Phe Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val
            175                 180                 185

act ttg aaa acg aaa tgc att ttg cct gta cac ctt tat gga aag ctg     1109
Thr Leu Lys Thr Lys Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu
        190                 195                 200

cct gac atg gaa gcc att gca aaa acc gct gat aaa tac ggc atc ccg     1157
Pro Asp Met Glu Ala Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro
    205                 210                 215

att att gaa gac gcc tgc cag gcg atc ggc gtt tcc gat ctg gga aaa     1205
Ile Ile Glu Asp Ala Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys
220                 225                 230                 235

aac agc ctt tgc tcc ata tta agc ttc aat ccg tat aaa aat ctc ggc     1253
Asn Ser Leu Cys Ser Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly
                240                 245                 250

act tgc gga aaa gcc ggc gca att gtg acg gat gat cca tca ttt gca     1301
Thr Cys Gly Lys Ala Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala
            255                 260                 265

tcc gca tgc atg gaa tat atg tat cac ggc ttt gaa ctg aat caa aaa     1349
Ser Ala Cys Met Glu Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys
        270                 275                 280

aat aaa aag gcg gct gac tac ggc ttt aac gct aag att gat aat ctg     1397
Asn Lys Lys Ala Ala Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu
    285                 290                 295

caa gcc gct att gga ctg gca agg atg aaa tat ctt tct tta aat aat     1445
Gln Ala Ala Ile Gly Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn
300                 305                 310                 315

ctg aag cgc tta tat tta gca gat cgt tat att gcg cat ttg cag cag     1493
Leu Lys Arg Leu Tyr Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln
                320                 325                 330

tat gaa gac aga ggt ctg atc aaa ttg cct caa atg acc gat gat cat     1541
Tyr Glu Asp Arg Gly Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His
            335                 340                 345

gta tgg cat ttg ttt aca att aaa ata cta aac gga aat cgt gac caa     1589
Val Trp His Leu Phe Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln
        350                 355                 360

gtc aaa gat atg atg ctt aaa ttt cat aat gtc caa aca gat ata tac     1637
Val Lys Asp Met Met Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr
    365                 370                 375
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tac ccg att tta tcc cat cat caa aac aca cca ctt gta aaa gcc aat      1685
Tyr Pro Ile Leu Ser His His Gln Asn Thr Pro Leu Val Lys Ala Asn
380                 385                 390                 395

tat cgg cac aca tca ctg ccg gtc act gaa tca gtg cat aaa caa atg      1733
Tyr Arg His Thr Ser Leu Pro Val Thr Glu Ser Val His Lys Gln Met
                400                 405                 410

ctt cag ctt cct ctc tat ccg ggg ctc acc gta gaa gaa caa gac aaa      1781
Leu Gln Leu Pro Leu Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys
            415                 420                 425

gta atg gag gcc tta att gat gtc gta tca tgaaacactt tcttttcaca        1831
Val Met Glu Ala Leu Ile Asp Val Val Ser
        430                 435

ccttgcagca agtaaacaag ccgaagtacg ccgtattttg cgattttgat gagacatatt    1891

tcgcccacag catcaccgat gaatcgagaa aagcgctcat ggaccttgaa acatttattc    1951

attcgcacca tcttgatcac aagattttgc tcggctgggt gaccgggagc agcctgtcat    2011

ccgttcttgc aaaaatgaag cggggaggct ttcgatatct tccgcatttt gtcgccggtg    2071

accttggcac tgaaatcact tatttctctg aagaaggcca agtctctgat aaagattggg    2131

aagcccgatt gcaagaatca aatttctccc atgatctggt cgaagaaatc aagcagactc    2191

tctctaaaaa atatgagatt gcgcttgtgc ctcagactca gcatggcttt tcccgctata    2251

aaatcaacta ttactataaa tcgttggaag agagcataga taagagggcg cttgaagcca    2311


<210>  161
<211>  437
<212>  PRT
<213>  Bacillus licheniformis

<400>  161

Met Lys Thr Ala Asn Glu Asn Met Thr Cys Thr Ser Lys Gln Leu Phe
1               5                   10                  15

Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu Ala Gly Glu Cys Arg
            20                  25                  30

Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys Glu Thr Leu Gln Gln
        35                  40                  45

Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn Arg Met Asp Ser Pro
    50                  55                  60

Pro Ser Arg Val Asp Phe Met Pro Leu His Arg Leu Ile Thr Glu Glu
65                  70                  75                  80

Glu Val Asp Asp Val Val His Ala Val Lys Asp Val Leu Pro Thr Gly
                85                  90                  95

Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe Glu Ala Glu Ile Ala
            100                 105                 110
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10295.204.ST25.txt

Ala Phe Leu Ser Lys Lys His Val Met Ala Ser Ser Ser Gly Thr Asp
115 120 125

Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val Gly Gln Gly Asp Glu
130 135 140

Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr Glu Asn Ala Val Leu
145 150 155 160

Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile Asp Pro Val Thr Phe
165 170 175

Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val Thr Leu Lys Thr Lys
180 185 190

Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu Pro Asp Met Glu Ala
195 200 205

Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro Ile Ile Glu Asp Ala
210 215 220

Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys Asn Ser Leu Cys Ser
225 230 235 240

Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly Thr Cys Gly Lys Ala
245 250 255

Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala Ser Ala Cys Met Glu
260 265 270

Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys Asn Lys Lys Ala Ala
275 280 285

Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu Gln Ala Ala Ile Gly
290 295 300

Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn Leu Lys Arg Leu Tyr
305 310 315 320

Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln Tyr Glu Asp Arg Gly
325 330 335

Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His Val Trp His Leu Phe
340 345 350

Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln Val Lys Asp Met Met
355 360 365

Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr Tyr Pro Ile Leu Ser
370 375 380

```
His His Gln Asn Thr Pro Leu Val Lys Ala Asn Tyr Arg His Thr Ser
385                 390                 395                 400

Leu Pro Val Thr Glu Ser Val His Lys Gln Met Leu Gln Leu Pro Leu
                405                 410                 415

Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys Val Met Glu Ala Leu
            420                 425                 430

Ile Asp Val Val Ser
        435

<210>  162
<211>  2143
<212>  DNA
<213>  Bacillus licheniformis

<220>
<221>  CDS
<222>  (501)..(1643)

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caaaacagca tcagacagca gctgtatgaa cgcattggtc ttccgcttga ccggtatgcg     120

gttttgattc atccctctgc tgttgtcagc ggttcggccc ggattcaaaa cggcgccgtt     180

gttatggcat cgagcgtcat ccaagcggat gcagacgtcg gcatccacgc gattgtcaac     240

acaggtgcga tcgtcgaaca cgacaatcgg atcggcgatt acgttcatct ttcgcccgga     300

acggtgttaa ccggcggcgt gacagttatg gaaggcgctc atctcggcgc gggaacggcg     360

gtcattcccg gaaagacagt cggacgctgg agcgtgacgg gagcgggggc agccgtgatt     420

cacgacattc ctgataattg caccgcagtc ggagtccctg caagaatgat caaataacag     480

cagtaaaaag ggtgaaaaac atg agt cag aat aag cga att tat tta tca ccg     533
                     Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro
                     1               5                   10

ccg cac atg agc gga gac gag gag cgc tat gta gcc gaa gcg ttt cgg       581
Pro His Met Ser Gly Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg
            15                  20                  25

aca aac tgg atc gcg ccc ctc ggt ccc ctt gtc gac aca ttt gaa gaa       629
Thr Asn Trp Ile Ala Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu
        30                  35                  40

aag ctt gcc gcc tat gcg ggg acg tcc gga gcc gcg gca gtc agc tca       677
Lys Leu Ala Ala Tyr Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser
    45                  50                  55

gga aca gct gcg atc cac ctg gcc ttg aaa ttg ctc ggc gtc ggc aaa       725
Gly Thr Ala Ala Ile His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys
60                  65                  70                  75

ggc gat acg gtc ttc tgc tct tct ttt acg ttt gta gcg agc gcc aat       773
Gly Asp Thr Val Phe Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn
                80                  85                  90

ccg atc ata tat gag cag gct gaa ccg gtt ttc att gat tct gaa cgg       821
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Pro Ile Ile Tyr Glu Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg
95 100 105

gat aca tgg aac atg tcg ccc gag gcg ctt gaa cgg gcg ctt gac gaa 869
Asp Thr Trp Asn Met Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu
110 115 120

gcg gag cgg gcc agg aat ctc ccg aaa gcc gtc atc gtc gtc aac ttg 917
Ala Glu Arg Ala Arg Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu
125 130 135

tac ggc caa agc gcg aaa atg gac gag att atg gcc att tgc gat cga 965
Tyr Gly Gln Ser Ala Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg
140 145 150 155

ttt gcc gtg cct gtc att gaa gat gca gcc gaa tcg ctc ggt tct gtt 1013
Phe Ala Val Pro Val Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val
160 165 170

tat aaa ggc aga aaa agc ggg acc ttc gga cgc ttc ggc att tat tcg 1061
Tyr Lys Gly Arg Lys Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser
175 180 185

ttc aac ggt aac aaa atc atc acc aca tcg ggc gga gga atg ctg gtc 1109
Phe Asn Gly Asn Lys Ile Ile Thr Thr Ser Gly Gly Gly Met Leu Val
190 195 200

agc gat gat gaa gac gcg ttg aag aag gcg cgc ttt tta gcc act cag 1157
Ser Asp Asp Glu Asp Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln
205 210 215

gcg cgc gag cca gcc att cat tat cag cac gaa aaa gcg ggc tac aat 1205
Ala Arg Glu Pro Ala Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn
220 225 230 235

tac cgg atg agc aat gtt ctg gcc gga atc ggc atc gca cag ctc gcc 1253
Tyr Arg Met Ser Asn Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala
240 245 250

gtt ctg gat gac cgg gta cat gcc aga cgg gcg gtt ttc gag cgc tat 1301
Val Leu Asp Asp Arg Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr
255 260 265

aag gag gcg ctt tcc ggt atc gaa ggt ata gaa ttc atg cct gag gcc 1349
Lys Glu Ala Leu Ser Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala
270 275 280

ggc atg tca aac cgc tgg ctc acg aca tta acg tta gac aca gca aag 1397
Gly Met Ser Asn Arg Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys
285 290 295

att caa aca aca ccg gcg gac atc atc gaa cag ctc gca aat gaa aac 1445
Ile Gln Thr Thr Pro Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn
300 305 310 315

att gag gcc cgc ccg tta tgg aag cct ttg cac aga cag ccc ctt ttt 1493
Ile Glu Ala Arg Pro Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe
320 325 330

aaa ggc gcg gcc ttt tat ccg cac gat gac cag ggc tct gtc tgc tgc 1541
Lys Gly Ala Ala Phe Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys
335 340 345

gac tta ttt cag cgc ggg ctc tgc ctg ccg tca gga tca agt atg acg 1589
Asp Leu Phe Gln Arg Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr
350 355 360

cga aaa gag cag gac cgg gta att caa atc gtt gcc gac cgg att aaa 1637

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Arg Lys Glu Gln Asp Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys
    365                 370                     375

tat aaa tgaggtgcta aacatggcga ttacatattc catggacagc ttaaagcata      1693
Tyr Lys
380

agctggcaga aattttggat gtcattccaa ggcattcatc agtcgtttac ttggactacc   1753

cgctatacgg aaacgtcggg gatctattga tcatgaaagg aacggaagct ttttttgaag   1813

catacggcat caaggtgcgc gaaagatgga atgcggagaa tttcattccg ggccgccgca   1873

ttccaaagga cgccatcatt gtttgtcagg ggggcggcaa tttcggcgac ttgtaccctc   1933

acttccagca gttcagagaa cgggtggtcg aacattaccc ggacaaccgg atcgtcattc   1993

tgccgcagtc gatttattat gagcatgaag aaaatataat aaaaacgcgc ggcattttgg   2053

cggctcaccc ggatctgcac ttattcacgc gggaaaaggc atcattcgat tttgccgtca   2113

agcgtttcga agaggtgaaa aacatcaaaa                                    2143


<210>  163
<211>  381
<212>  PRT
<213>  Bacillus licheniformis

<400>  163

Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro Pro His Met Ser Gly
1               5                   10                  15

Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg Thr Asn Trp Ile Ala
            20                  25                  30

Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu Lys Leu Ala Ala Tyr
        35                  40                  45

Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser Gly Thr Ala Ala Ile
    50                  55                  60

His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys Gly Asp Thr Val Phe
65                  70                  75                  80

Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn Pro Ile Ile Tyr Glu
                85                  90                  95

Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg Asp Thr Trp Asn Met
            100                 105                 110

Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu Ala Glu Arg Ala Arg
        115                 120                 125

Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu Tyr Gly Gln Ser Ala
    130                 135                 140

Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg Phe Ala Val Pro Val
```

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145                 150                 155                 160

Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val Tyr Lys Gly Arg Lys
                165                 170                 175

Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser Phe Asn Gly Asn Lys
            180                 185                 190

Ile Ile Thr Thr Ser Gly Gly Gly Met Leu Val Ser Asp Asp Glu Asp
        195                 200                 205

Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln Ala Arg Glu Pro Ala
    210                 215                 220

Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn Tyr Arg Met Ser Asn
225                 230                 235                 240

Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala Val Leu Asp Asp Arg
                245                 250                 255

Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr Lys Glu Ala Leu Ser
            260                 265                 270

Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala Gly Met Ser Asn Arg
        275                 280                 285

Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys Ile Gln Thr Thr Pro
    290                 295                 300

Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn Ile Glu Ala Arg Pro
305                 310                 315                 320

Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe Lys Gly Ala Ala Phe
                325                 330                 335

Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys Asp Leu Phe Gln Arg
            340                 345                 350

Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr Arg Lys Glu Gln Asp
        355                 360                 365

Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys Tyr Lys
    370                 375                 380

&lt;210&gt;  164
&lt;211&gt;  2107
&lt;212&gt;  DNA
&lt;213&gt;  Bacillus licheniformis

&lt;220&gt;
&lt;221&gt;  CDS
&lt;222&gt;  (501)..(1607)
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aggcgggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat 180

tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaatg 240

tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg 300

aggaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa 360

ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt ttttttatga 420

ataaaatcaa gccgtgccaa tttagcggca ggcatcataa cttattttgg aacttttga 480

atttagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt 533
Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe
1 5 10

caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac 581
Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp
15 20 25

agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga 629
Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg
30 35 40

ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga 677
Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly
45 50 55

acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg 725
Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly
60 65 70 75

gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc 773
Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala
80 85 90

gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa 821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu
95 100 105

aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct 869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala
110 115 120

act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg 917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met
125 130 135

gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag 965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu
140 145 150 155

gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag cgg cct gtc ggc 1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly
160 165 170

agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg 1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu
175 180 185

gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca 1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala

190 195 200

gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac 1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr
205 210 215

ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc 1205
Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala
220 225 230 235

gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa 1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln
240 245 250

aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag 1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu
255 260 265

cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat 1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His
270 275 280

ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg 1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu
285 290 295

aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat 1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His
300 305 310 315

ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct 1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro
320 325 330

ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct 1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro
335 340 345

ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa 1589
Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys
350 355 360

aaa gga gga ggg gaa aag tgacggttca ttttggttta atcggctgcg 1637
Lys Gly Gly Gly Glu Lys
365

gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg 1697

ccgtcagtga tttgcaggaa gaaagaatga aggaagcgga agaatactat gcttccctcg 1757

ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta 1817

aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg 1877

cgctgctggc aggcaagcac gtcatcgtcg aaaaaccgat gaccttgtca ttacgggatg 1937

ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga 1997

tgcgccaccg gccgatcatg aaaaaactga aggaaacgat tgaggaagga aagctgggaa 2057

agatctactt gggcacggta tcgctccgct taaacaggtc cccgcttat 2107

<210> 165
<211> 369
<212> PRT
<213> Bacillus licheniformis

<400> 165

Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe Gln Thr Val Lys Gln
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Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile
20 25 30

Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
65 70 75 80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
260 265 270

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
275 280 285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
355 360 365

Lys

<210> 166
<211> 2092
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1592)

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ggctattata agcatgacct gatcatcggt tcaaacagct ggatcgggca gcaatgtttt 180

atacacggtg ccggcggggt tacaatcgga gaatttgcag gaattggtcc gaacgtccgg 240

atacatgccg cttaccatac cgatcctgat aaacccgaca gtaccatttt gttttcgccg 300

cttacattcg ctcctattca tattgaagaa aactgcaaca tcgggatcgg tgcgtctatc 360

ctagcaggcg ttacgatagg cgcccactcc aaaatcggag caaatgccgt cgtcaatcgc 420

aatattcccc cgtacagcat agcagtaggc gtgccggcaa aggtgattaa aaaccgaaga 480

atgaaagatg aggatctctc atg atc aga ttg atc gag ccg tat att aca ttt 533
Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe
1 5 10

gaa gaa gtg caa gca gaa tta aag gag ata ttt tcc tct ggc atg ctg 581
Glu Glu Val Gln Ala Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu
15 20 25

aca aaa ggc cct tat gtc aga aca ttt gct gat cat atg aga cag tat 629
Thr Lys Gly Pro Tyr Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr
30 35 40

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gtc agt gca aag cat gct ttt tta aca aca tcg gca aca acg gct tta      677
Val Ser Ala Lys His Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu
    45                  50                  55

tcg atg tgc ctt aaa agc ctg aac gtg caa ccc gga gat gaa gta atc      725
Ser Met Cys Leu Lys Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile
60                  65                  70                  75

gtc tca gac ttc tcg ttc ccc gcc act gtc aat gta ata gaa gat tta      773
Val Ser Asp Phe Ser Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu
                80                  85                  90

gga gcc aag ccg gtt ttt gcc gat gtt gat ctt gaa aca ttt aac atg      821
Gly Ala Lys Pro Val Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met
            95                  100                 105

ctt cca gaa gaa ctg gaa agt caa atc acg tcc cgt aca aaa gcc gtt      869
Leu Pro Glu Glu Leu Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val
        110                 115                 120

ctt ttt gta gat gct ctt gga aac ccg aca ggc atc acc aac att aag      917
Leu Phe Val Asp Ala Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys
    125                 130                 135

caa att tgt aag gag tac ggc tta ccc ctt gtg gat gat gcc gct tgt      965
Gln Ile Cys Lys Glu Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys
140                 145                 150                 155

gcg atc ggc agc agc gaa tac ggc tgt aaa tcc gga aaa att gcc gat     1013
Ala Ile Gly Ser Ser Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp
                160                 165                 170

ctc acc tgt ttc agc ttt cac cca aga aag ctg ctt acg aca ggc gaa     1061
Leu Thr Cys Phe Ser Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu
            175                 180                 185

ggc ggg gca att aca acc gac cgg gaa gag ttg aaa gac tgg ctt tcg     1109
Gly Gly Ala Ile Thr Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser
        190                 195                 200

gtc aaa tta aac cat ggc gct gcc atc tct gac gga aaa ttg gat ttt     1157
Val Lys Leu Asn His Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe
    205                 210                 215

ata gat ttc ggc tac aac tac aga tta tcc gat atc caa gcc gct ctt     1205
Ile Asp Phe Gly Tyr Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu
220                 225                 230                 235

gga att aaa cag ctc caa aaa ctt gat gac atc att cat cgg aga aac     1253
Gly Ile Lys Gln Leu Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn
                240                 245                 250

ctt cag cag aaa gca tat agt gaa cag ctt gaa ccc ctc gga ttc caa     1301
Leu Gln Gln Lys Ala Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln
            255                 260                 265

agt caa aaa atc ggt cca gcc gtt gta cac aac ata caa tcc gcc gtt     1349
Ser Gln Lys Ile Gly Pro Ala Val Val His Asn Ile Gln Ser Ala Val
        270                 275                 280

ttc aaa gtt cca aaa aac atc gtt cgc gac gaa ttg att caa tat ttg     1397
Phe Lys Val Pro Lys Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu
    285                 290                 295

agc gac tgc cat ata gag tcg act ttc ggc act tat tgt tta agc ggc     1445
Ser Asp Cys His Ile Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly
300                 305                 310                 315
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act ccc tat tac cgc cgg aaa tac caa cag cta aaa tcg aat tct ctc      1493
Thr Pro Tyr Tyr Arg Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu
                320                 325                 330

ttt ctt gaa caa cat acg att acc ctc cct tgc cat gat gaa gtc gat      1541
Phe Leu Glu Gln His Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp
            335                 340                 345

tta gat cat gtg gtt tca gcc ata caa tca ttt atc aaa ttt aag gtt      1589
Leu Asp His Val Val Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val
        350                 355                 360

gat tagttcaaaa tatcccgttc acagagaata gtgaacggga tattttttat          1642
Asp

tcttaataca agaataaaaa aacaggtagt aaaccataga tttaccacct gattcattca   1702
cataacaata cagcgaactt ccatgaaaaa aaacattcac ctgtagatta agagacagtt   1762
ggaccgagaa tatatgcaaa tctgttagaa tgaaaatgct agtggaatat tcgatgtttt   1822
tacaagcatc gtttaatatt tggacagaca atgtgtaact ctcaattgta caattagttt   1882
tctttaaaga gaaactgctc cgcaagaaaa acctacggaa cagcttccta atgagaatat   1942
taattagaaa gtttttcgat ttggatatga ccgctgtttc ctgtagcaag agttaacgct   2002
aatccagtga cggcaatctg aatagtagaa gggacagcag taacttcaat catagcttct   2062
cccactaatg gagtacctac gctgattaaa                                   2092


<210>  167
<211>  364
<212>  PRT
<213>  Bacillus licheniformis

<400>  167

Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe Glu Glu Val Gln Ala
1               5                   10                  15

Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu Thr Lys Gly Pro Tyr
            20                  25                  30

Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr Val Ser Ala Lys His
        35                  40                  45

Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu Ser Met Cys Leu Lys
    50                  55                  60

Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile Val Ser Asp Phe Ser
65                  70                  75                  80

Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu Gly Ala Lys Pro Val
                85                  90                  95

Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met Leu Pro Glu Glu Leu
            100                 105                 110
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Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val Leu Phe Val Asp Ala
        115                 120                 125

Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys Gln Ile Cys Lys Glu
    130                 135                 140

Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys Ala Ile Gly Ser Ser
145                 150                 155                 160

Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp Leu Thr Cys Phe Ser
                165                 170                 175

Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu Gly Gly Ala Ile Thr
            180                 185                 190

Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser Val Lys Leu Asn His
        195                 200                 205

Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe Ile Asp Phe Gly Tyr
    210                 215                 220

Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu Gly Ile Lys Gln Leu
225                 230                 235                 240

Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn Leu Gln Gln Lys Ala
                245                 250                 255

Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln Ser Gln Lys Ile Gly
            260                 265                 270

Pro Ala Val Val His Asn Ile Gln Ser Ala Val Phe Lys Val Pro Lys
        275                 280                 285

Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu Ser Asp Cys His Ile
    290                 295                 300

Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly Thr Pro Tyr Tyr Arg
305                 310                 315                 320

Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu Phe Leu Glu Gln His
                325                 330                 335

Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp Leu Asp His Val Val
            340                 345                 350

Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val Asp
        355                 360
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<210> 168
<211> 1663
<212> DNA

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<213>  Bacillus licheniformis


<220>
<221>  CDS
<222>  (501)..(1163)

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tggtttccgg ttcatcaaac acagctgctc ctcgtatttt tcatcgggct gtcggcagcc     120

ggcatttttc cgtgcgccgt cactcttgcc tcgttggctg gaaagccttt tacagaggaa     180

atcacgagtc tcttcatttc gtccgcaagt ctgggaggag cgcttctttc attcttgatc     240

ggctgggcga ttgatgcaag cgcagccgct gtcttcccgt ttttgctgtt cggcggattg     300

gggggcttgc tgctggcgat cagcgcggtg atttttttat ccggcctgca aaaaaacaag     360

cagagtcatt tggatatgta gatttattag gaagagatta caagcttagt aggatttttt     420

tcagcagccg tttaaaccgt tccatctttg accataatat tgctagaaaa ggttgaagaa     480

cgagaggaac ggtggggaaa atg aag aaa tca aac att gcc tgt atg tat att     533
                      Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile
                      1               5                   10

ttt ctt tta tta ata gga gcg ctt gca aat ctc acg acg gaa gag act       581
Phe Leu Leu Leu Ile Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr
            15                  20                  25

gcc caa tca tca ggc ggg cag cct gcc gtg att cct gat gaa gcg att       629
Ala Gln Ser Ser Gly Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile
        30                  35                  40

cgg ctg cgg att ttg gca aac agc gac agc ggg agc gac cag agc gtc       677
Arg Leu Arg Ile Leu Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val
    45                  50                  55

aaa cgc aaa atc agg gat gag gtc aat aaa caa att acg aaa tgg gtg       725
Lys Arg Lys Ile Arg Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val
60                  65                  70                  75

gaa aac ctg acc tcg gtt gag gaa gcg aga caa gtc atc agg tcg aag       773
Glu Asn Leu Thr Ser Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys
                80                  85                  90

ctg cct gaa atc caa gag gtt gcc atg gat gtc atg aaa cgc gaa aat       821
Leu Pro Glu Ile Gln Glu Val Ala Met Asp Val Met Lys Arg Glu Asn
            95                  100                 105

gtt cgg caa tcc gtg tct gtc cgt ttt gat cgt gtt tca ttt ccg aca       869
Val Arg Gln Ser Val Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr
        110                 115                 120

aag cta tac ggc aat atg gtg tat ccg gcc gga gaa tat gag gct gtt       917
Lys Leu Tyr Gly Asn Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val
    125                 130                 135

tta att aca tta ggc aag gga gag gga gcc aac tgg tgg tgc gtc ctg       965
Leu Ile Thr Leu Gly Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu
140                 145                 150                 155

ttt ccg cca ctt tgc ttt ctt gat ttt tcc aat ggg gaa gcc gta aag      1013
Phe Pro Pro Leu Cys Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys
                160                 165                 170
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tcg cct gaa gac gaa caa acc gct gcc gga gaa gac cgc cgg gaa gaa      1061
Ser Pro Glu Asp Glu Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu
            175                 180                 185

aaa aca gac gcg gcg gat gaa acg gta tct ggc ata gat aaa gat aaa      1109
Lys Thr Asp Ala Ala Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys
        190                 195                 200

gaa gac aaa gaa gtg aaa ttt ttt ctt gtc gaa tgg att acc ggg ctt      1157
Glu Asp Lys Glu Val Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu
    205                 210                 215

ttt tct taaaaggacc gccttgcttt cgtgtgcagg gcggtttttt actgtttgtt       1213
Phe Ser
220

ttttcatgat ggttattgaa gcttttgaat atgatataat tttccaaaac ggttcagggg    1273

aaatactgct tttcggatat acaccttttg cccctttctg atgtgccaat cacattgccg    1333

gcagaagaga aactgtctta tcaccagtac agcgttcatt tgcatactca ttcaaagcgt    1393

tggttcctgc taatcaaaat tgaaaaatga atagccggca ttcttccaaa tcaaaaggta    1453

tattttactg tcgccctcat agattggata gagaagttaa aaaacggggt gaaaagatgt    1513

tctaccaatt gaggttagcg gaaacgaaag acatgaatgc gatcgaagca tttttaaaaa    1573

aggcggggac aagccataag ggtcttgagg aagcgaagag ccagtttatc atgatggaag    1633

accctcccga tgaaatcgtc gcctgcctcg                                     1663


<210>  169
<211>  221
<212>  PRT
<213>  Bacillus licheniformis

<400>  169

Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile Phe Leu Leu Leu Ile
1               5                   10                  15

Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr Ala Gln Ser Ser Gly
            20                  25                  30

Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile Arg Leu Arg Ile Leu
        35                  40                  45

Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val Lys Arg Lys Ile Arg
    50                  55                  60

Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val Glu Asn Leu Thr Ser
65                  70                  75                  80

Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys Leu Pro Glu Ile Gln
                85                  90                  95

Glu Val Ala Met Asp Val Met Lys Arg Glu Asn Val Arg Gln Ser Val
            100                 105                 110
```

Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr Lys Leu Tyr Gly Asn
115 120 125

Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val Leu Ile Thr Leu Gly
130 135 140

Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu Phe Pro Pro Leu Cys
145 150 155 160

Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys Ser Pro Glu Asp Glu
165 170 175

Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu Lys Thr Asp Ala Ala
180 185 190

Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys Glu Asp Lys Glu Val
195 200 205

Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu Phe Ser
210 215 220

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<211> 1351
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<213> Bacillus licheniformis

<220>
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<222> (501)..(851)

<400> 170
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cgttcagcca atatgaaacg catccgatgt ataaacgtaa cgaaatcatt tccgatttga 120

aggtcaataa aggccgtgag caaaaaataa accttgtcac atcagaaccg atttcccttt 180

tgacgaaaaa aggcgaaaat atcgaatctg ttaaaaaaga aatcaaacag aaagaagata 240

tccaggcccc tgtcaaaaaa ggcacagagc ttgggacgct cgttttgaaa aaggatggaa 300

aggtgctcgc tgaaagtcct cttgtcgctg aaaaagatat ggacaaagcg gggatgtgga 360

cgatgttcaa gcggacgatg acccactgga cgaagtggag tgaataatgc cgaacggtca 420

ctagttttgt cacggtgaag gaatttataa agtctgaagc gaaacactca ttatccgatt 480

taaaccaagg aggaatgagg atg agc ctc gga atc gat att cac gtc aaa gaa 533
Met Ser Leu Gly Ile Asp Ile His Val Lys Glu
1 5 10

tcc gta tta tgc att cgg ttg aca ggt gaa ctc gat cac cat aca gca 581
Ser Val Leu Cys Ile Arg Leu Thr Gly Glu Leu Asp His His Thr Ala
15 20 25

gaa acc ttg aga aaa caa gtc agt gac cat ctg gaa caa acc gac att 629
Glu Thr Leu Arg Lys Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile
30 35 40

cgc cat att gtc atg aat ctt gca gac ctt tcg ttt atg gac agt tca 677

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Arg His Ile Val Met Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser
    45                  50                      55

ggg ctt ggc gtc gtg ctc ggc aga tat aag gag att aag cag ctc ggc      725
Gly Leu Gly Val Val Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly
60                  65                  70                  75

gga gaa atg atc gtc tgc gcc att tcc cct gct gtc aaa cgt tta ttt      773
Gly Glu Met Ile Val Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe
                80                  85                  90

gat atg tcc ggg ctg ttt aaa atc att cgc ctt gag caa tca gag cag      821
Asp Met Ser Gly Leu Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln
            95                  100                 105

cgt gca ctt gaa acg ttg ggg gtg gcg tca tgaaaaatga aatgaacatt        871
Arg Ala Leu Glu Thr Leu Gly Val Ala Ser
        110                 115

cagtttacag cgctcagcca aaatgaatcg tttgcacggg tgacagtcgc tgcttttatc    931

gctcagcttg acccgacgat ggatgaactg accgaaatta aaacggtcgt atccgaagcg    991

gtcacaaacg cgatcattca cggttatgaa aactcagggc agggaaacgt atatatttcc    1051

gtcactctcg aggaccatat tgtctattta acgatccgcg acgaaggagt cggcatccct    1111

aatcttgaag aagcgcgcca gcccctgttc acgacaaagc ctgaactcga gcggtcggga    1171

atgggcttta cgatcatgga aaatttcatg gatgatattt cgatcgactc ctcacctgag    1231

atgggaacca caatacactt aacaaagcac ttatcaaaaa gcaaagcgct ttgcaattaa    1291

gggagatttg ttatggatgt ggaggttaaa aaagaaaacc agaacactca gcttaaagac    1351

<210>  171
<211>  117
<212>  PRT
<213>  Bacillus licheniformis

<400>  171

Met Ser Leu Gly Ile Asp Ile His Val Lys Glu Ser Val Leu Cys Ile
1               5                   10                  15

Arg Leu Thr Gly Glu Leu Asp His His Thr Ala Glu Thr Leu Arg Lys
            20                  25                  30

Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile Arg His Ile Val Met
        35                  40                  45

Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser Gly Leu Gly Val Val
    50                  55                  60

Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly Gly Glu Met Ile Val
65                  70                  75                  80

Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe Asp Met Ser Gly Leu
                85                  90                  95

Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln Arg Ala Leu Glu Thr
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        100                       105                       110

Leu Gly Val Ala Ser
        115


<210>  172
<211>  1438
<212>  DNA
<213>  Bacillus licheniformis


<220>
<221>  CDS
<222>  (501)..(938)

<400>  172
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ttatccgatt taaaccaagg aggaatgagg atgagcctcg gaatcgatat tcacgtcaaa     180

gaatccgtat tatgcattcg gttgacaggt gaactcgatc accatacagc agaaaccttg     240

agaaaacaag tcagtgacca tctggaacaa accgacattc gccatattgt catgaatctt     300

gcagaccttt cgtttatgga cagttcaggg cttggcgtcg tgctcggcag atataaggag     360

attaagcagc tcggcggaga aatgatcgtc tgcgccattt cccctgctgt caaacgttta     420

tttgatatgt ccgggctgtt taaaatcatt cgccttgagc aatcagagca gcgtgcactt     480

gaaacgttgg gggtggcgtc atg aaa aat gaa atg aac att cag ttt aca gcg     533
                      Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala
                      1               5                   10

ctc agc caa aat gaa tcg ttt gca cgg gtg aca gtc gct gct ttt atc       581
Leu Ser Gln Asn Glu Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile
            15                  20                  25

gct cag ctt gac ccg acg atg gat gaa ctg acc gaa att aaa acg gtc       629
Ala Gln Leu Asp Pro Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val
        30                  35                  40

gta tcc gaa gcg gtc aca aac gcg atc att cac ggt tat gaa aac tca       677
Val Ser Glu Ala Val Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser
    45                  50                  55

ggg cag gga aac gta tat att tcc gtc act ctc gag gac cat att gtc       725
Gly Gln Gly Asn Val Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val
60                  65                  70                  75

tat tta acg atc cgc gac gaa gga gtc ggc atc cct aat ctt gaa gaa       773
Tyr Leu Thr Ile Arg Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu
                80                  85                  90

gcg cgc cag ccc ctg ttc acg aca aag cct gaa ctc gag cgg tcg gga       821
Ala Arg Gln Pro Leu Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly
            95                  100                 105

atg ggc ttt acg atc atg gaa aat ttc atg gat gat att tcg atc gac       869
Met Gly Phe Thr Ile Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp
        110                 115                 120

tcc tca cct gag atg gga acc aca ata cac tta aca aag cac tta tca       917
Ser Ser Pro Glu Met Gly Thr Thr Ile His Leu Thr Lys His Leu Ser
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    125                 130                 135

aaa agc aaa gcg ctt tgc aat taagggagat ttgttatgga tgtggaggtt        968
Lys Ser Lys Ala Leu Cys Asn
140                 145

aaaaaagaaa accagaacac tcagcttaaa gaccatgaag tgaaagaact gattaaaaac   1028

agccagaacg gcgatcaaaa agcaagggac ctcctcatag aaaaaaacat gcgtcttgtt   1088

tggtctgtcg ttcagcgttt tttgaacaga ggctatgagc ctgacgacct ctttcaaatc   1148

ggctgcatcg gcctcttgaa gtcggtggac aaattcgatc tttcctatga cgttcggttt   1208

tccacctacg ccgttccgat gattatcggc gagattcagc ggtttatcag agatgacgga   1268

accgtcaaag tgagccgctc gctgaaagaa ctcggcaaca aaatccggcg ggcgaaagac   1328

gagctttcca agtcaaacgg ccggattccg accgttcagg aaatcgccga ttatctcgaa   1388

atcagttcag aagaggtcgt gatggcccag gaagcggtcc gctctccctc              1438
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<210> 173
<211> 146
<212> PRT
<213> Bacillus licheniformis

<400> 173

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Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala Leu Ser Gln Asn Glu
1               5                   10                  15

Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile Ala Gln Leu Asp Pro
            20                  25                  30

Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val Val Ser Glu Ala Val
        35                  40                  45

Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser Gly Gln Gly Asn Val
    50                  55                  60

Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val Tyr Leu Thr Ile Arg
65                  70                  75                  80

Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu Ala Arg Gln Pro Leu
                85                  90                  95

Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly Met Gly Phe Thr Ile
            100                 105                 110

Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp Ser Ser Pro Glu Met
        115                 120                 125

Gly Thr Thr Ile His Leu Thr Lys His Leu Ser Lys Ser Lys Ala Leu
    130                 135                 140

Cys Asn
145
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<210> 174
<211> 5482
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(4982)

<400> 174
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ccatgaagag cctgacgctt caagtcgatc cgaataattt cctttactgg attcagatcg 120

gacgcggcgc caataaagaa gcgcttgaga cggcccgtaa gctggaaaac aatgcacaga 180

tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg 240

atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattg aagcggacag 300

cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg 360

cggacgtaga ggccgcaaag gctgaaacgg agaaggccga gaaggaacag gcgaaaaaag 420

aaaataaaga aaaggaagac aaaaagaaaa aagatgacaa ataaaagcga aaacacctgt 480

tgttggcagg aggcggagaa atg agt ctg tta tgg att ttt tat cat aaa aac 533
Met Ser Leu Leu Trp Ile Phe Tyr His Lys Asn
1 5 10

tat caa aaa ata aaa ctg gat gat cag aac agc cgc acg ctc acc atc 581
Tyr Gln Lys Ile Lys Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile
15 20 25

ggg ccg gat ttg aaa cat tct gtc acg att aag cat ttt tca ttt gaa 629
Gly Pro Asp Leu Lys His Ser Val Thr Ile Lys His Phe Ser Phe Glu
30 35 40

aaa ggc ccg gtg aca ctg gaa aag cag aag gac tca gac gct ttg aac 677
Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn
45 50 55

gtg cag ctg gga ggg gag acg gtc tct tct tta aag ctt ggc gga aag 725
Val Gln Leu Gly Gly Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys
60 65 70 75

gcg tcc gtc caa agc ggc gct gaa cag ctg acg ctc ttt tta gcc gaa 773
Ala Ser Val Gln Ser Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu
80 85 90

gaa gcc gac agc gtt cct gcc tac tat ttg gga gag aga cag gaa atc 821
Glu Ala Asp Ser Val Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile
95 100 105

gtc att tct tcc ctc gat caa gaa gcg gat gtt tat ttc aat gaa acg 869
Val Ile Ser Ser Leu Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr
110 115 120

gat tca ttc ttt gga gaa aaa ggt acg ttc tct ttc atc cgc ctc gac 917
Asp Ser Phe Phe Gly Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp
125 130 135

ggg caa tgg aat gtc ctg ccg aat gac gcg aaa att tat ttg aac gga 965
Gly Gln Trp Asn Val Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly
140 145 150 155

gaa gaa gtg tcc gcc cct gtc tcc gtg caa aat gga gac gaa atc gca 1013
Glu Glu Val Ser Ala Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala
160 165 170

ttt gga ctg aat att ctt cgc atc gtt gaa gac gac ctc ttg gaa atc 1061
Phe Gly Leu Asn Ile Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile
175 180 185

gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg 1109
Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro
190 195 200

agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga 1157
Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg
205 210 215

atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca 1205
Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala
220 225 230 235

cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct 1253
Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro
240 245 250

ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg 1301
Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro
255 260 265

cgg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg 1349
Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu
270 275 280

att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa 1397
Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys
285 290 295

aga gaa gaa aaa aga gag cgg gtc tat acc ctt tac ctt gaa aac aaa 1445
Arg Glu Glu Lys Arg Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys
300 305 310 315

aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat 1493
Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp
320 325 330

ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc 1541
Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile
335 340 345

agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa 1589
Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln
350 355 360

atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg 1637
Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu
365 370 375

aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa 1685
Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln
380 385 390 395

acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc 1733
Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile
400 405 410

act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc 1781
Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser
415 420 425

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gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc      1829
Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe
        430                 435                 440

cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag      1877
His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu
    445                 450                 455

tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct      1925
Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro
460                 465                 470                 475

cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag      1973
His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln
                480                 485                 490

ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa      2021
Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu
            495                 500                 505

aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca      2069
Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr
        510                 515                 520

aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc      2117
Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly
    525                 530                 535

aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa      2165
Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys
540                 545                 550                 555

gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa      2213
Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu
                560                 565                 570

cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg      2261
Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro
            575                 580                 585

ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc cgg      2309
Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg
        590                 595                 600

acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct      2357
Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro
    605                 610                 615

gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac      2405
Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp
620                 625                 630                 635

atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg      2453
Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu
                640                 645                 650

gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac      2501
Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn
            655                 660                 665

ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc      2549
Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr
        670                 675                 680

ggt tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca      2597
Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala
    685                 690                 695
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gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa 2645
Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys
700 705 710 715

ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga 2693
Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly
720 725 730

acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt 2741
Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu
735 740 745

gcg tcc att aag agc gag ctg aag aaa agg cag cgg ctc ttt gat cag 2789
Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln
750 755 760

tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa 2837
Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys
765 770 775

aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt 2885
Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe
780 785 790 795

gcc gag ctg aaa agc gaa gaa ccg gaa ttt atc cgc gag ctt gtc agt 2933
Ala Glu Leu Lys Ser Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser
800 805 810

gcg gca agg atc ggg cga agc ctc ggg gtg cac tta atc ttg gcg acg 2981
Ala Ala Arg Ile Gly Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr
815 820 825

caa aaa ccg ggc ggc atc atc gat gac cag att tgg agc aac tcc aga 3029
Gln Lys Pro Gly Gly Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg
830 835 840

ttc aag gtc gcc ttg aag gtg cag gat gcg aat gac agt aaa gag atc 3077
Phe Lys Val Ala Leu Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile
845 850 855

ctc aaa aac ggg gat gcg gct acc atc acg gta acg ggc cgc ggc tat 3125
Leu Lys Asn Gly Asp Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr
860 865 870 875

ttg caa gtc ggc aac aac gag gtg tat gaa ctg ttc cag tct gca tgg 3173
Leu Gln Val Gly Asn Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp
880 885 890

agc gga gcc cct tac atg gag gac ggc tac ggc aca gag gat gaa gtg 3221
Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val
895 900 905

gcg atc gtc aca gat acc gga tta att cct tta tca gat gtt gat gct 3269
Ala Ile Val Thr Asp Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala
910 915 920

gat cgc gct gcg aaa aaa gag gct gtg acg gaa att tcg gca gtc gtc 3317
Asp Arg Ala Ala Lys Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val
925 930 935

gaa caa att gaa cgg att caa gcg gag atg gga atc gag aag ctc ccg 3365
Glu Gln Ile Glu Arg Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro
940 945 950 955

agc cct tgg ctg ccg ccg ctt gaa gaa cgc ata ccg aaa acg cgc tat 3413
Ser Pro Trp Leu Pro Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr
960 965 970

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ccg tcg gag gaa gcc gat gcc ttt aac ttt gcc tat atc gat gaa cct      3461
Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro
            975                 980                 985

gaa aag caa agc cag gag ccg atc agc tac cgc atg atg gaa gac ggc      3509
Glu Lys Gln Ser Gln Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly
        990                 995                 1000

aat atc ggc atc gtc ggc tcg tca ggc tac gga aaa tcc ctg aca          3554
Asn Ile Gly Ile Val Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr
    1005                1010                1015

gcc acg acg ttc atg atg agc ttt gcc gaa cag tat acg ccg gaa          3599
Ala Thr Thr Phe Met Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu
    1020                1025                1030

gaa ttg cat tac tac att ttc gac ttt ggc aac gga acg ctg ctt          3644
Glu Leu His Tyr Tyr Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu
    1035                1040                1045

ccg ctt gca agg ctt ccg cac acc gcg gat tat ttc ctg atg gac          3689
Pro Leu Ala Arg Leu Pro His Thr Ala Asp Tyr Phe Leu Met Asp
    1050                1055                1060

caa acg aga aaa atc gag aaa ttt atg gtc cgg atc aag gcg gaa          3734
Gln Thr Arg Lys Ile Glu Lys Phe Met Val Arg Ile Lys Ala Glu
    1065                1070                1075

atc gag cac agg aaa aat ctc ttc cgt gca aaa gaa atc agc cat          3779
Ile Glu His Arg Lys Asn Leu Phe Arg Ala Lys Glu Ile Ser His
    1080                1085                1090

atc aag atg tac aat gcg ctg aat gag gaa aag ctg ccg ttt att          3824
Ile Lys Met Tyr Asn Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile
    1095                1100                1105

ttc ata acg gtc gac aac ttt gac atc att aaa gac gaa atg cat          3869
Phe Ile Thr Val Asp Asn Phe Asp Ile Ile Lys Asp Glu Met His
    1110                1115                1120

gaa ctc gaa agc gaa ttt atc cag ttt tca cga gac ggc cag tcg          3914
Glu Leu Glu Ser Glu Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser
    1125                1130                1135

ctt gga att tat tta atc ctg acc gcg aca agg gtc aat gca atc          3959
Leu Gly Ile Tyr Leu Ile Leu Thr Ala Thr Arg Val Asn Ala Ile
    1140                1145                1150

aga cag tcg ctc ttg aac aac ctg aaa acg agg gtt gtc cac tat          4004
Arg Gln Ser Leu Leu Asn Asn Leu Lys Thr Arg Val Val His Tyr
    1155                1160                1165

ctg atg gat cag tct gaa gca tat tcg att atc gga agg ccg gaa          4049
Leu Met Asp Gln Ser Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu
    1170                1175                1180

ttc agc ctt gaa ccg atc cct gga cgc gtt att atc aat aaa gaa          4094
Phe Ser Leu Glu Pro Ile Pro Gly Arg Val Ile Ile Asn Lys Glu
    1185                1190                1195

aac caa tac ttc gca caa atg ttt atg cct gtg gaa gcg gac aac          4139
Asn Gln Tyr Phe Ala Gln Met Phe Met Pro Val Glu Ala Asp Asn
    1200                1205                1210

gat atc gag ctg ttt gaa ggg atc aaa gcc gac att cag gcg atc          4184
Asp Ile Glu Leu Phe Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile
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gca gaa cgc tcg gaa ggc atg aga aag ccg gcg cct gtg ccg atg 4229
Ala Glu Arg Ser Glu Gly Met Arg Lys Pro Ala Pro Val Pro Met
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ctg ccg ctc gag ctt tcc gtc aca cag ttt gtg aga gat tat ccg 4274
Leu Pro Leu Glu Leu Ser Val Thr Gln Phe Val Arg Asp Tyr Pro
1245 1250 1255

ctt cag cct gaa aga ggc ctt att cca atg gga ctc gat gaa gaa 4319
Leu Gln Pro Glu Arg Gly Leu Ile Pro Met Gly Leu Asp Glu Glu
1260 1265 1270

act gtc gaa ccc gta tac ttt aat ctt gag aaa aat aag cac tgc 4364
Thr Val Glu Pro Val Tyr Phe Asn Leu Glu Lys Asn Lys His Cys
1275 1280 1285

ctc att atg ggt cag acg cag cgc gga aaa aca aac gtc atc aag 4409
Leu Ile Met Gly Gln Thr Gln Arg Gly Lys Thr Asn Val Ile Lys
1290 1295 1300

atc atg ctc gag cac ctg ctt gac cat gac acg aaa aaa atc gcc 4454
Ile Met Leu Glu His Leu Leu Asp His Asp Thr Lys Lys Ile Ala
1305 1310 1315

gtg ttt gat tcg ata gac aga ggg ctt tct caa tat gcg aca gag 4499
Val Phe Asp Ser Ile Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu
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gat caa atc agc tat cta gaa aca aaa gac gac att ctg ctc tgg 4544
Asp Gln Ile Ser Tyr Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp
1335 1340 1345

ctc gct gag acg gaa gaa att tgc cgg aca agg gaa gcg atg tat 4589
Leu Ala Glu Thr Glu Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr
1350 1355 1360

ttg gaa gcc gtt aaa caa gga gaa atc gcc aac ctt gat ttc tca 4634
Leu Glu Ala Val Lys Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser
1365 1370 1375

ccg atg gtc ttt att gtc gac gga att tca cgg ttc cag cag acg 4679
Pro Met Val Phe Ile Val Asp Gly Ile Ser Arg Phe Gln Gln Thr
1380 1385 1390

atc gac gca tcg att cag gac aaa atg gcg atg ttc atg aaa tct 4724
Ile Asp Ala Ser Ile Gln Asp Lys Met Ala Met Phe Met Lys Ser
1395 1400 1405

tac gcc cat tta ggt ttc cac ttt ata cct gcc gga aat cac agc 4769
Tyr Ala His Leu Gly Phe His Phe Ile Pro Ala Gly Asn His Ser
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gag ttc aca aaa ggc tat gat tcg ctg aca agc gaa gtc aag cag 4814
Glu Phe Thr Lys Gly Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln
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gtc aga cac gcg atg cta ttg atg aaa aaa tcc gag cag aac ttg 4859
Val Arg His Ala Met Leu Leu Met Lys Lys Ser Glu Gln Asn Leu
1440 1445 1450

att cag ctc cca tat gaa cgc cag gag ccg gaa att ctg ccg ggc 4904
Ile Gln Leu Pro Tyr Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly
1455 1460 1465

ttt ggc tat atc gtt gaa aac ggc aaa gag agg aaa att caa att 4949
Phe Gly Tyr Ile Val Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile
1470 1475 1480

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cct tta  tgt gct gta gaa agg  aag aaa gcg aaa tgacggaaca          4992
Pro Leu  Cys Ala Val Glu Arg  Lys Lys Ala Lys
    1485                 1490

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gtttttcat ttcatcggtg agaacccgac gaaaaaggta tcgaacgcga caagggaaat  5112

cgccgttgtc aatgaggata ccggcgtttt gaaagatgac ggaaccgttg atcaagatgc  5172

gctgctggga aacgaaatct cggcttccct ggttgaccgt ccggattata aatggacggt  5232

cgtcaaccgg agcgcagcag aaagcggact tgcggagaag caatacgatg cgattgtcta  5292

cattccgtcg gacttttcgc aaaacatttt aagctacaac catgagcgtc cgcaaaaagc  5352

ggagctggaa ttcaaaattc aggaccagct cgacgccgtc aacaaggaaa aagtccagcg  5412

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His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
        35                  40                  45

Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
    50                  55                  60

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
65                  70                  75                  80

Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
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Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
            100                 105                 110

Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
        115                 120                 125

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
    130                 135                 140

Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala
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Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
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Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
180 185 190

Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
195 200 205

Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
210 215 220

Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
225 230 235 240

Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
245 250 255

Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
260 265 270

Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
275 280 285

Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys Arg Glu Glu Lys Arg
290 295 300

Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys Lys Lys Glu Leu His
305 310 315 320

Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
325 330 335

Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile Ser Gly Arg Ile Trp
340 345 350

Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
355 360 365

Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
370 375 380

Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
385 390 395 400

Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile Thr Val Asn Leu Ala
405 410 415

Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu

420 425 430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
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Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
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Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
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Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
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Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
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Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
515 520 525

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
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Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
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Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
580 585 590

His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro

690 695 700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala
705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
785 790 795 800

Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly
805 810 815

Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
820 825 830

Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
835 840 845

Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
850 855 860

Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
865 870 875 880

Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
885 890 895

Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
900 905 910

Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
915 920 925

Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
930 935 940

Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
945 950 955 960

Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala

965 970 975

Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln
980 985 990

Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
995 1000 1005

Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr Ala Thr Thr Phe Met
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Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu Glu Leu His Tyr Tyr
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Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
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Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys
1070 1075 1080

Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn
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Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
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Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
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Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
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Asn Asn Leu Lys Thr Arg Val Val His Tyr Leu Met Asp Gln Ser
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Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu Phe Ser Leu Glu Pro
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Gln Met Phe Met Pro Val Glu Ala Asp Asn Asp Ile Glu Leu Phe
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Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile Ala Glu Arg Ser Glu

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Gly Met Arg Lys Pro Ala Pro Val Pro Met Leu Pro Leu Glu Leu
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Ser Val Thr Gln Phe Val Arg Asp Tyr Pro Leu Gln Pro Glu Arg
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Gly Leu Ile Pro Met Gly Leu Asp Glu Glu Thr Val Glu Pro Val
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Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
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Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu Asp Gln Ile Ser Tyr
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Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp Leu Ala Glu Thr Glu
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Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr Leu Glu Ala Val Lys
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Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser Pro Met Val Phe Ile
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Val Asp Gly Ile Ser Arg Phe Gln Gln Thr Ile Asp Ala Ser Ile
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Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly
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Phe His Phe Ile Pro Ala Gly Asn His Ser Glu Phe Thr Lys Gly
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Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln Val Arg His Ala Met
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gaatataatc gaacaaaaca aggacgcaca ggaagggata atccaatgat tctgtatacg 180

aaaatgccgc aggaaatcgt gttcgcaggg caggcggaaa actcgaaatt aaaacagatc 240

gatgtaaaca gcgtgccact tttagtcgag atgaacggag aggaagcaag ggacgttcag 300

gttctcagca cgaacccgat ggattttta aaacaagaaa cggcccctgg gcagacgctt 360

aaactgacat tttataaata gctggagtgt ctcaaggata aatatgctat aatagggggaa 420

tccagaggaa aatcgcagcc gaaaaaaggc tgctttctct ttgtttttac attttttaac 480

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Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys
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caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga 581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly
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tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta 629
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val
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gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg 677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp
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ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt 725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe
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Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu
80 85 90

tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt 821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe
95 100 105

cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa 869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln
110 115 120

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Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser

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Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu
                160                     165                 170

atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg       1061
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ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg       1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp
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cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa       1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys
    205                     210                 215

aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct       1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser
220.                    225                 230                 235

gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa       1253
Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln
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Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu
            255                     260                 265

gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag       1349
Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu
        270                     275                 280

ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg       1397
Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr
    285                     290                 295

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Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu
300                     305                 310                 315

ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att       1493
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Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val
            335                     340                 345

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Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr
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Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu
    365                     370                 375

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Ser Asp Asp Leu Ala Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu
380                     385                 390                 395

gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg       1733
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Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser
        430                 435                     440

gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt        1877
Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val
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Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile
460                 465                     470                     475

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Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met
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Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His
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Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu
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aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac        2117
Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His
    525                 530                     535

acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg        2165
Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met
540                 545                     550                     555

aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg        2213
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                560                     565                     570

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Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val
            575                 580                     585

gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc        2309
Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile
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His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly
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Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser
620                 625                     630                     635

cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt        2453
Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu
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Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro
            655                 660                     665

ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt        2549
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670 675 680

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685 690 695

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700 705 710 715

tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta 2693
Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val
720 725 730

tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg 2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg
735 740 745

ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga 2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly
750 755 760

tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc 2837
Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu
765 770 775

tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac 2893
Ser Ser
780

atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat 2953

ctgatctgtc agacggaggg aaaacatgtc gataaaagct gacatcaacg gttatgttta 3013

aaggtgattg atcggataaa agatgatatt caaaatgggg tcttttgcga aaatgaacgg 3073

ctcccgagtg aatttgagct gtcaaagatg cttggtgtga gcagaacggc tttgcgtgag 3133

gcgcttagaa tactggaaga agaaaacgtc atcatcagaa ggcatggagt cggacatttt 3193

gtaaatgcca gaccgttatt tctatcaggt attgagcagc tgaacagcgt cacaaaaatg 3253

atcgagcagg caagcatgac gccgggaacc atttttatgt cctcacaggt taccgctccc 3313

actgaagaag atatgctccg gtttcaatat 3343

<210> 177
<211> 781
<212> PRT
<213> Bacillus licheniformis

<400> 177

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys
1 5 10 15

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala
20 25 30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe
35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
50 55 60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
145 150 155 160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
165 170 175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
180 185 190

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
325 330 335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
420 425 430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
435 440 445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
450 455 460

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
530 535 540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
580 585 590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
595 600 605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780

<210> 178
<211> 1735
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1235)

<400> 178
gatattgtgc gtaaacacta tcttccgatc cggtgaagac gagttcgacg tcgggattct 60

gttttgcaaa ctgctcaaac cgttgtttaa ttgcagtctg gcctttctct ttgtacgctt 120

tttgatcaat ccattcgctg aaatacgcaa tggaagtctc cttgctgccg atatcttgct 180

gaataatgtc gttcagttca tcgatattgt ctttcgcact tctcaaaatc tcatcctcga 240

gcgtgctgct ggccgtaaaa tatgaagtaa ccgaaagaac caagatcgga attgttaaaa 300

tgaatataaa tgagaaaatt aattttttag aaatagaagg acgtttcgtc caatttaaaa 360

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gctttttcat gtgtgattcc cctttctcta cttttatcgg agacggggtc tattttttaa      420

ataaaaaaag cggaaaatta gaccgttttc ctgcccaagc atcaggcata cgctaataaa      480

aaaggaaaag ggtgtatcct atg ata agt gtt tcg ggc tac cgg ctc cgt cct      533
                      Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro
                      1               5                   10

gag gat atc gaa aaa ctg aat gtc agt cag acg cag aga gac atc gca        581
Glu Asp Ile Glu Lys Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala
            15                  20                  25

aac cgg atg ctg gcc atg ccg tcc gga tat aga tac ggt tca atc tca        629
Asn Arg Met Leu Ala Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser
        30                  35                  40

gaa ctg tta ttt gag ctg aga ttc aga gag cat acc gtc aaa tcg gcc        677
Glu Leu Leu Phe Glu Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala
    45                  50                  55

aga gag ctg atc aac agc gga gcg aag ttt gcc acc ttt tca aag aca        725
Arg Glu Leu Ile Asn Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr
60                  65                  70                  75

tac ggg aat gaa gag ttt tgg agg gtg acg cct gag ggg gct ttg gag        773
Tyr Gly Asn Glu Glu Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu
                80                  85                  90

ttg aag tac agg gca ccg gct tca aag gcg att cga aat att ttt gaa        821
Leu Lys Tyr Arg Ala Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu
            95                  100                 105

agc ggc cct tct tat gct ttt gag tgc gcg act gcg att gtc atc att        869
Ser Gly Pro Ser Tyr Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile
        110                 115                 120

ttt tat atg gcg ctt ctc aaa acg atc ggc gac cag aca ttt gac cgg        917
Phe Tyr Met Ala Leu Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg
    125                 130                 135

aat tat caa agg atc att tta tac gat tgg cac tat gag cgg ctg ccg        965
Asn Tyr Gln Arg Ile Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro
140                 145                 150                 155

atc tat acg gat aaa gga aac gac tac ctt ccg gga gac tgc ctg tat       1013
Ile Tyr Thr Asp Lys Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr
                160                 165                 170

ttc aag aac cct gaa ttc gat ccc tca aga ccg cag tgg cgc gga gaa       1061
Phe Lys Asn Pro Glu Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu
            175                 180                 185

aat gct att tta ctt gaa aat aat ctc tat gcg gca cac ggc ctg ggg       1109
Asn Ala Ile Leu Leu Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly
        190                 195                 200

atc tta agc ggc gaa aca atc att gaa aaa ctg aac ggg ctg aga aag       1157
Ile Leu Ser Gly Glu Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys
    205                 210                 215

cct cat gca cag acg tcc gcc tat ctg ctt tcc caa gtg acg cgg gtt       1205
Pro His Ala Gln Thr Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val
220                 225                 230                 235

gat att ccg gca tta att caa atg atc aga tagcacatcg gccggcacaa         1255
Asp Ile Pro Ala Leu Ile Gln Met Ile Arg
                240                 245
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gctgatccat cagctccttc accgtcgttt gctcgacggt ggcccgcacg ctctgtccgg 1315

cccacaatga catgttatcc gtattcccgt caagcttcgc ctgttttctc atcggttgcg 1375

tcagcgtgtt ttgcagagga taaggcagcg cttcagcttc ttcctggcgt ctgtcttcca 1435

tccactgatt gacgatgcct cttgccggct tccccgagaa caaacgggtc aggcttgtgt 1495

cggtttcaac cgcttcgaac aatttttgtt tgtaggcagg gtgtgttccg ctttcttcgc 1555

acgtcaaaaa agcggtaccg atttgaacgc cctgtgcgcc gagggcaaaa gctgcagcaa 1615

cacctctttt gtcaaaaatg ccgcccgctg cgataactgg aaccgacaca tgatctgccg 1675

cttggggaat taaagccatc gagccgacag caggctctcc cttcgttttc aagaaggctc 1735

<210> 179
<211> 245
<212> PRT
<213> Bacillus licheniformis

<400> 179

Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro Glu Asp Ile Glu Lys
1   5   10   15

Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala Asn Arg Met Leu Ala
            20   25   30

Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser Glu Leu Leu Phe Glu
        35   40   45

Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala Arg Glu Leu Ile Asn
    50   55   60

Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr Tyr Gly Asn Glu Glu
65   70   75   80

Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu Leu Lys Tyr Arg Ala
                85   90   95

Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu Ser Gly Pro Ser Tyr
            100   105   110

Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile Phe Tyr Met Ala Leu
        115   120   125

Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg Asn Tyr Gln Arg Ile
    130   135   140

Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro Ile Tyr Thr Asp Lys
145   150   155   160

Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr Phe Lys Asn Pro Glu
                165   170   175

Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu Asn Ala Ile Leu Leu
180 185 190

Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly Ile Leu Ser Gly Glu
195 200 205

Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys Pro His Ala Gln Thr
210 215 220

Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val Asp Ile Pro Ala Leu
225 230 235 240

Ile Gln Met Ile Arg
245

<210> 180
<211> 1405
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(905)

<400> 180
aggctatact acagtctgag gtgattgaaa ttggccaaac gaaaagcaaa tcatgtaata 60

aatggaatga acaatgcgaa acgccaagga aacggcgcgg gatatattga aaatgatcag 120

cacatactca ctgaggcgga acgccaaaac aacaaaaaac ggaaaaccaa tcaataaata 180

cgaaagatcc ttcatgaata tcttaggagg ttaaaacatt gacaaataaa aacgacggca 240

aagatatgcg caaaaacgca ccgaaaggag ctcagccggg gcagccagag cctttgagcg 300

gaagcaaaaa agtaaaaaac cggaaccata caagacaaaa acacaattcc agtcacgata 360

tgtaacattt tttccgcgcc tttcacggcg cggttttttt ccttaccgcg cgtcaccctg 420

aggcgttgtc caccctcctt cacatgaatt caaaggtgtg cataatctaa tggtaaggct 480

aggtatggag gaatgctcca atg aca aat aca aaa cgt ttc gat tcc gca gat 533
Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp
1 5 10

ttt gat aaa gaa tgg atg aaa cag ttt gtt gac gac cct ttt ctc ctc 581
Phe Asp Lys Glu Trp Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu
15 20 25

tat gat gaa act tta ccg att gac ctt tat gaa acg agc act gaa tat 629
Tyr Asp Glu Thr Leu Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr
30 35 40

ata att gaa gca gat tta agc cac ttg aat gtc cgg cat ctt gac ttg 677
Ile Ile Glu Ala Asp Leu Ser His Leu Asn Val Arg His Leu Asp Leu
45 50 55

acg ttt tca ggc tac gat ttc aag ctt gca gtt aaa acc gat gag cag 725
Thr Phe Ser Gly Tyr Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln
60 65 70 75

ctt tac gag aaa tcg ctg atg ctt cct ttc ttt ttg aat gac aaa cag 773
Leu Tyr Glu Lys Ser Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln
80 85 90

atc gaa gcg gaa tgc gaa aac aac att ctt gca gtt aaa atc aat aaa 821
Ile Glu Ala Glu Cys Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys
95 100 105

gaa tca agc aaa gat gac att tcg ctt tca atc aat att cct ttt ata 869
Glu Ser Ser Lys Asp Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile
110 115 120

tca aac ctg cac aac aag cag aac ccg gac agc gct taaaacactt 915
Ser Asn Leu His Asn Lys Gln Asn Pro Asp Ser Ala
125 130 135

gccatccggg tttttttccg ttcgttcgtc aaatatcctc tagcaattct ctatggccga 975

ttagggaatc gctatacaat agattatgtt ctagcatctc ttttgaccag gccggtgtcc 1035

cattttatat tattttttct atgttcttct aaaacgcctt catgtaaaat aggttataga 1095

caaaggagtg atgagagatg ctggaaggat ggtttttatg gctgatgctc gcttggatcg 1155

tcatcatgat cgtcctcttg tcaatcggcg gtttttttcat gtttcgcaaa tttttaaaaa 1215

ggctgcctaa agaagatggg aaatctgagc tggactggca ggattattat attgaacaga 1275

caaggcattt gtggaatgac gaagaaaaag aactgcttga ggaattggtt tcacccgtac 1335

ccgagctgtt tcgcgatgta gcaaaagcaa aaatcgccgg taagatcggg gagcttgcat 1395

tgaaagaaaa 1405

<210> 181
<211> 135
<212> PRT
<213> Bacillus licheniformis

<400> 181

Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp Phe Asp Lys Glu Trp
1 5 10 15

Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu Tyr Asp Glu Thr Leu
20 25 30

Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr Ile Ile Glu Ala Asp
35 40 45

Leu Ser His Leu Asn Val Arg His Leu Asp Leu Thr Phe Ser Gly Tyr
50 55 60

Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln Leu Tyr Glu Lys Ser
65 70 75 80

Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln Ile Glu Ala Glu Cys
85 90 95

Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys Glu Ser Ser Lys Asp
100 105 110

Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile Ser Asn Leu His Asn
115 120 125

Lys Gln Asn Pro Asp Ser Ala
130 135

<210> 182
<211> 2155
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1655)

<400> 182
aaaggttttc agaaagcttc ggcgtttctt ttgatgagct gatgacagcg gccggctatg 60

cgatggagaa gacgcaggaa agcgaacgtc cggatattca ctcgtcagtt gccgaaattg 120

aagatgtttt gcaaacctca aatgtctatg atcggccatt taccatggaa gaactgaaaa 180

acaaattgaa tgagtgcgaa caatattctc agacggagga aggaaagcgt accattctgg 240

ctgagtttga atctaaaatc gagaaagttg ccggcattgg tccttttctg acccgtctgc 300

acgacatgta cagcagattt acctcggggc gggggacgcc gcgtgaattg ctgctgatgg 360

gcggcgcttt gctgtatttc atcgtttctg ttgatgtcat accggattat atttttccga 420

tcggctatat cgatgatgcg gcagcggttc atttcgtttt caaccagctg tcatataaat 480

catgatggag catgttcaag atg aaa aga aag cat atc aac att gac atc agt 533
Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser
1 5 10

ctg ctg ctc att cta ttt tgt ttg ttt atc atc agc ctg ctg gcc gtt 581
Leu Leu Leu Ile Leu Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val
15 20 25

tac agc ggg tcg ggc cag tat gaa aca cag gac cct ttt tat ttt gcc 629
Tyr Ser Gly Ser Gly Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala
30 35 40

aaa cgg cag gtc ttt tgg tat ctt gtc ggg ttt ggc gtc atg gcg gga 677
Lys Arg Gln Val Phe Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly
45 50 55

acg gcc tac atc gac tat gag ctg ctt gaa cga ttg gcg ctt cgt tta 725
Thr Ala Tyr Ile Asp Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu
60 65 70 75

ttt gtg gga gcc gtt ttt ctt ctg att ctc gtt cat ttt ttt gga act 773
Phe Val Gly Ala Val Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr
80 85 90

tac aaa aac ggt tcg caa agg tgg atc agc ttc ggg gtc atc gaa atc 821
Tyr Lys Asn Gly Ser Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile
95 100 105

cag cct tca gaa ttt atg aag atc att ttg att ctt ctg ctg gct tcg 869
Gln Pro Ser Glu Phe Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser
110 115 120

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ata ctc aat caa ttt cag cat aaa agg ttc tcc ttc gcc gag agc atc        917
Ile Leu Asn Gln Phe Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile
    125                 130                 135

att ccg acg gga aaa atc atg atg tac acg gtg att ccg ttt ttc ttt        965
Ile Pro Thr Gly Lys Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe
140                 145                 150                 155

ata ttg gtt cag cca gat tta ggg tcc gca ttg gtg att tta tcg atc       1013
Ile Leu Val Gln Pro Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile
                160                 165                 170

gca ttc acg ttg atg ctg gtc tcg ggg att tcg ggc agg atg atc gtg       1061
Ala Phe Thr Leu Met Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val
            175                 180                 185

tcc ctg tca ctt gga ttc atg gca ttg gtt gcc ttt ttg acg tat ttg       1109
Ser Leu Ser Leu Gly Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu
        190                 195                 200

cac aat cat tac ttt gag ata ttt tca aag att att aag cct cac cag       1157
His Asn His Tyr Phe Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln
    205                 210                 215

ctt gac cgg ata tat ggc tgg ctc agt cct cat gaa cat gcc tct aca       1205
Leu Asp Arg Ile Tyr Gly Trp Leu Ser Pro His Glu His Ala Ser Thr
220                 225                 230                 235

tat gga tac cag ctg acg cag gcg tta ttg ggg atc gga tca ggc cag       1253
Tyr Gly Tyr Gln Leu Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln
                240                 245                 250

ctg tca ggg agc ggc ttt act caa gga atc caa gtt cag gga ggg aaa       1301
Leu Ser Gly Ser Gly Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys
            255                 260                 265

att ccg gag gct cat act gat ttt att ttc gcc gtg att ggt gag gaa       1349
Ile Pro Glu Ala His Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu
        270                 275                 280

ttc ggt ttt ttg ggt gcc gta aca tta gtc tgt ctg tat ttt ctg atg       1397
Phe Gly Phe Leu Gly Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met
    285                 290                 295

atc tac aga atc atc agg att gcg ctt tcg tcc aac agt ctg ttc ggt       1445
Ile Tyr Arg Ile Ile Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly
300                 305                 310                 315

ctt tat ata tgt gcg ggg gtt gca ggg ttg att gta ttc caa gtg ttc       1493
Leu Tyr Ile Cys Ala Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe
                320                 325                 330

caa aat atc ggg atg acg atc ggg tta atg ccg atc acg ggg ctc gct       1541
Gln Asn Ile Gly Met Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala
            335                 340                 345

ctt ccg ttt atc agc tat ggc ggc agc gcg ctg ttg acc aac atg atc       1589
Leu Pro Phe Ile Ser Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile
        350                 355                 360

gct tta ggt ctc gtt ttc agt gtg aat atc aga tct aaa cat tac atg       1637
Ala Leu Gly Leu Val Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met
    365                 370                 375

ttt ggg aat gat tgg gga tgaagttgct caaaatgatt ctttcccatc              1685
Phe Gly Asn Asp Trp Gly
380                 385
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taaagaaact tgattatgta ttgattgccg cggttctgtt tttatctgcg tttggcttgc 1745

tgatggtata cagcgccggc taccccctcg gatatatgaa gtatcatgat ggcagctatt 1805

tttttatgaa gcagctgcaa tggctgctca tcggtttggc ctttttttcg gctgccgcca 1865

ttttcccata caaagcttac agcaaactca ttcggttttt ggtgaagctt tctttttttaa 1925

tgctgattct cgttttgctg ccgggaatcg ggatggagaa aaacaattcc caaaggtgga 1985

ttcaattcgg ttcgctcatg attcagccgt ctgaggctgt gaagcttgtg atggttattt 2045

atttcgccta tgtgtatgca aaaaagcaga aatacatcgc cgatttcgga aagggcgtca 2105

tgccgccgct gctgattttg gcggctgtgt ttttttgat tttaaaacag 2155

<210> 183
<211> 385
<212> PRT
<213> Bacillus licheniformis

<400> 183

Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser Leu Leu Leu Ile Leu
1 5 10 15

Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val Tyr Ser Gly Ser Gly
20 25 30

Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala Lys Arg Gln Val Phe
35 40 45

Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly Thr Ala Tyr Ile Asp
50 55 60

Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu Phe Val Gly Ala Val
65 70 75 80

Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr Tyr Lys Asn Gly Ser
85 90 95

Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile Gln Pro Ser Glu Phe
100 105 110

Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser Ile Leu Asn Gln Phe
115 120 125

Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile Ile Pro Thr Gly Lys
130 135 140

Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe Ile Leu Val Gln Pro
145 150 155 160

Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile Ala Phe Thr Leu Met
165 170 175

Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val Ser Leu Ser Leu Gly
180 185 190

Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu His Asn His Tyr Phe
195 200 205

Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln Leu Asp Arg Ile Tyr
210 215 220

Gly Trp Leu Ser Pro His Glu His Ala Ser Thr Tyr Gly Tyr Gln Leu
225 230 235 240

Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln Leu Ser Gly Ser Gly
245 250 255

Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys Ile Pro Glu Ala His
260 265 270

Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu Phe Gly Phe Leu Gly
275 280 285

Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met Ile Tyr Arg Ile Ile
290 295 300

Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly Leu Tyr Ile Cys Ala
305 310 315 320

Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe Gln Asn Ile Gly Met
325 330 335

Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala Leu Pro Phe Ile Ser
340 345 350

Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile Ala Leu Gly Leu Val
355 360 365

Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met Phe Gly Asn Asp Trp
370 375 380

Gly
385

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<213> Bacillus licheniformis

<220>
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<222> (501)..(1613)

<400> 184

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gacgaaaaaa gcgctgtccg cctttcaaaa gccggtcatt ttgctggcag gggggcttga     180
ccgcggaaat gaatttgatg aactaaagcc gcatatgtct tttgtaaaag cggtgatcac     240
tttcggcgag accgcgccga agtttgagaa gctggccgaa gaaatgggaa tacaacaggt     300
taaacgtgtc gataatgttg aacaagcagc aactgcggcg ttcagcctgt cagacgaagg     360
agatgtcatt cttctgtccc cggcctgcgc aagctgggat cagtacaaaa catttgaaga     420
acgtggtgac atgtttgtaa acgccgtgca tatgcttaaa taagggcttg tctcgtaaag     480
atagccctaa gaattagagc ttg ggg tgt tcg gct ttg caa aca aaa aaa acg     533
                      Leu Gly Cys Ser Ala Leu Gln Thr Lys Lys Thr
                      1               5                   10

tca ccg gat ttt ttg ctg gtt atc att acg cta ttg ctt tta aca atc       581
Ser Pro Asp Phe Leu Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile
            15                  20                  25

gga ctg att atg gta tac agc gcc agt gca gta tgg gcg act tac aaa       629
Gly Leu Ile Met Val Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys
        30                  35                  40

tac gac gac tcc ttt ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc       677
Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly
    45                  50                  55

atc ggg gtc atc gcc atg ttt ttc atc atg aac gtc gac tac tgg acg       725
Ile Gly Val Ile Ala Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr
60                  65                  70                  75

tgg agg act tat gcg aaa ata ctg atc att gta tgt ttc ttt ctg ctc       773
Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu
                80                  85                  90

atc atc gtc ctg gtt ccc ggg atc ggc atg gaa cgg aac ggg tcg agg       821
Ile Ile Val Leu Val Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg
            95                  100                 105

agc tgg atc gga gtc ggc gct ttc agc att cag ccg tcc gag ttt atg       869
Ser Trp Ile Gly Val Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met
        110                 115                 120

aaa ctc gcg atg atc gca ttt ttg gcc aag ttt tta tct gaa aag caa       917
Lys Leu Ala Met Ile Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln
    125                 130                 135

aag aat att acg tcg ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att       965
Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile
140                 145                 150                 155

gtc ttt tca gct ttt ctg atc atc atg atg cag cct gac ctc gga aca      1013
Val Phe Ser Ala Phe Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr
                160                 165                 170

gga acc gtg atg gtc ggc aca tgc atc att atg atc ttt gtc gcg ggg      1061
Gly Thr Val Met Val Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly
            175                 180                 185

gcg aga att tcg cac ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt      1109
Ala Arg Ile Ser His Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly
        190                 195                 200
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ttt gtc ggc ctt gtg ctg tcg gcg ccg tac cgg atc aaa agg atc act      1157
Phe Val Gly Leu Val Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr
    205                 210                 215

tca tac ttg aac cct tgg gag gac cct tta gga agc ggc ttt caa atc      1205
Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile
220                 225                 230                 235

att cag tct ctt tat gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc      1253
Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly
                240                 245                 250

ctc ggc cag agc agg caa aag ttt ttc tat ctg cct gag ccg cag aca      1301
Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr
            255                 260                 265

gat ttt att ttt gcg att tta tca gag gag ctc ggc ttt atc ggc gga      1349
Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly
        270                 275                 280

tcg ctg att ctt ttg ctc ttc agc gtt cta tta tgg aga ggc atc aga      1397
Ser Leu Ile Leu Leu Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg
    285                 290                 295

atc gcg ctc ggt gcg ccc gat tta tac ggc agt ttt gtc gcc gtc ggc      1445
Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly
300                 305                 310                 315

gtc att tcg atg ata gcg att cag gtt atg atc aat atc gga gtc gtg      1493
Val Ile Ser Met Ile Ala Ile Gln Val Met Ile Asn Ile Gly Val Val
                320                 325                 330

act ggt ttg att cct gtt aca ggc att acg ctt ccg ttt tta agc tat      1541
Thr Gly Leu Ile Pro Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr
            335                 340                 345

ggc ggt tca tca ctg acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg      1589
Gly Gly Ser Ser Leu Thr Leu Met Leu Met Ala Val Gly Val Leu Leu
    350                 355                 360

aat gtc agc agg tat tct aga tac tagattttgg cgataaccct gttgcgagat    1643
Asn Val Ser Arg Tyr Ser Arg Tyr
    365                 370

agcagggtta tcggcgtgta cataaggatt aagggggaga acagatgcgg attgttgtta    1703

gcggaggcgg aacgggcggc catatttacc ccgcccttgc gtttattaaa gaagtgaaac    1763

ggcatcacga agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata    1823

tcgtcgagcg ggaagggatc cctttcaaag cgattgaaat tacgggtttt aaaagaaaac    1883

tttcatttga aaacgtcaaa accgtcatgc gctttttaaa gggtgtaaaa gaatgcaaag    1943

aagaattaaa acggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc    2003

ccgtcgtata cgccgcttca aaactgggga ttccgacgat tatccacgaa caaaacagcc    2063

ttcccggact caccaataag tttttatcca aatatgttga taaggtagcg               2113
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<210> 185
<211> 371
<212> PRT
<213> Bacillus licheniformis

<400> 185

Leu Gly Cys Ser Ala Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu
1 5 10 15

Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val
20 25 30

Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe
35 40 45

Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala
50 55 60

Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala
65 70 75 80

Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val
85 90 95

Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val
100 105 110

Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile
115 120 125

Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser
130 135 140

Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe
145 150 155 160

Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val
165 170 175

Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His
180 185 190

Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val
195 200 205

Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro
210 215 220

Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr
225 230 235 240

Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
245 250 255

Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
260 265 270

Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
275 280 285

Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
290 295 300

Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
305 310 315 320

Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
325 330 335

Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
340 345 350

Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
355 360 365

Ser Arg Tyr
370

<210> 186
<211> 2040
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1976)

<400> 186
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aaggcgacat taaagtggat taccggatgg atttggccaa gctgatgaag aagtcgaaaa 180

aaacggtaaa gccgggcgag gaagtccaag atttgatgtg ggaagagacg cctttcgttc 240

cggcgttttc ggtaaagtac acagtgaatg acaaacagga acctgttttt ctcgaataga 300

atatcggtca aaatgcaagt atcagtcatg aacctttctc ctcggcatac aatgaggaga 360

aaggtttttt catgtatgcc gaaaaaattt ccctaagctg tcatattgaa ataggacaac 420

gtcatacact atagtgtcct gtttttgatt gatgaagaag taaaaaattg aaaaggattg 480

gaagtccggg aggggatcac ttg gaa aag gtc gat att ttc aag gat atc gct 533
Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala
1 5 10

gaa cga aca gga ggc gat ata tac tta ggt gtc gta gga gct gta cgt 581
Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg
15 20 25

aca gga aaa tct acg ttt atc aaa aaa ttt atg gag cta gtg gtg ctc 629
Thr Gly Lys Ser Thr Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu
30 35 40

ccg aat atc aac aat gaa gca gac cgg gcg cgc gca caa gat gag ctc 677

Pro Asn Ile Asn Asn Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu
45 50 55

ccc caa agt gcc gct ggc aaa acc att atg aca act gaa ccg aag ttt 725
Pro Gln Ser Ala Ala Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe
60 65 70 75

gtt ccg aat cag gca atg tca gtt cat gtc agt gac gga ctc gat gtg 773
Val Pro Asn Gln Ala Met Ser Val His Val Ser Asp Gly Leu Asp Val
80 85 90

aat ata agg ctt gtc gac tgc gtc ggc tat act gta ccc ggg gca aag 821
Asn Ile Arg Leu Val Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys
95 100 105

gga tac gag gat gaa aac ggg ccg aga atg atc aat act cct tgg tat 869
Gly Tyr Glu Asp Glu Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr
110 115 120

gaa gag ccg att ccg ttt cac gaa gct gcc gaa atc ggc acg aga aaa 917
Glu Glu Pro Ile Pro Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys
125 130 135

gtc atc caa gag cac tcc aca atc ggt gtt gtg att acg act gac ggc 965
Val Ile Gln Glu His Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly
140 145 150 155

acg att gga gaa atc gcc aga cag gat tat gtc gag gct gaa gaa cgg 1013
Thr Ile Gly Glu Ile Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg
160 165 170

gtg atc gac gag ttg aaa gag gtt gga aaa ccg ttt atc atg gtc atc 1061
Val Ile Asp Glu Leu Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile
175 180 185

aat tcc gta agg ccg tat cat ccg gaa aca gaa gcg ctc agg caa gaa 1109
Asn Ser Val Arg Pro Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu
190 195 200

ttg atg gaa aag tac gac att ccg gtg ctg gcg atg agc gtt gaa agc 1157
Leu Met Glu Lys Tyr Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser
205 210 215

atg agg gaa gcg gac gtt ctg agc gtt ctc aga gaa gcg ctt tac gaa 1205
Met Arg Glu Ala Asp Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu
220 225 230 235

ttc cct gtg ctc gaa gtc aac gtc aat ctt cca agc tgg gtg atg gta 1253
Phe Pro Val Leu Glu Val Asn Val Asn Leu Pro Ser Trp Val Met Val
240 245 250

tta aaa gag aat cat tgg ctc agg gaa aac tat caa gat tcc gtt aaa 1301
Leu Lys Glu Asn His Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys
255 260 265

gaa acc gtc aaa gat att aaa aga ctg aga gat gtc gac cgc gtc gtc 1349
Glu Thr Val Lys Asp Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val
270 275 280

gga cac ttc agc gaa ttt gat ttc atc gag cgc gca agc ctc gcc gga 1397
Gly His Phe Ser Glu Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly
285 290 295

att gaa atg ggc cag ggg atc gcg gaa atc gat tta tac gcg ccg gat 1445
Ile Glu Met Gly Gln Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp
300 305 310 315

tac ctg tac gat gaa att ttg agg gaa gtc gtc ggc gtt gaa atc aga 1493

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Tyr Leu Tyr Asp Glu Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg
                320                 325                 330

gga aaa gat cac ctc ctt cag ctc atg cag gat ttt gcc cat gcc aag      1541
Gly Lys Asp His Leu Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys
            335                 340                 345

acc gaa tat gat caa gtc tca gat gca ttg aaa atg gtg aaa caa acc      1589
Thr Glu Tyr Asp Gln Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr
        350                 355                 360

ggc tat gga atc gca gct ccc gca tta acc gat atg agc ctg gat gaa      1637
Gly Tyr Gly Ile Ala Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu
    365                 370                 375

ccg gaa atc atc agg cag ggt tca aga ttc gga gtc cgg ctg aag gcg      1685
Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala
380                 385                 390                 395

gtg gcg ccg tcg att cat atg atc aaa gtc gat gtg gaa agc gag ttt      1733
Val Ala Pro Ser Ile His Met Ile Lys Val Asp Val Glu Ser Glu Phe
                400                 405                 410

gcg ccg atc atc gga aca gag aag cag agc gaa gag ctt gtc cgc tat      1781
Ala Pro Ile Ile Gly Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr
            415                 420                 425

tta atg cag gac ttt gag gac gat ccg ctg tca atc tgg aat tcc gac      1829
Leu Met Gln Asp Phe Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp
        430                 435                 440

ata ttc gga aga agc ttg agc tcg atc gtc aga gaa ggg att cag gcg      1877
Ile Phe Gly Arg Ser Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala
    445                 450                 455

aag ctg tca ctc atg cct gaa aat gcg aga tat aag ctg aag gag acg      1925
Lys Leu Ser Leu Met Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr
460                 465                 470                 475

ctg gag cgc att atc aat gaa ggc tca ggc ggc ttg att gcg atc atc      1973
Leu Glu Arg Ile Ile Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile
                480                 485                 490

tta taaaagggaa ggcctcttat catacgggag gtcttttttt atgcctgaaa           2026
Leu

acaggctgaa cggg                                                      2040


&lt;210&gt;  187
&lt;211&gt;  492
&lt;212&gt;  PRT
&lt;213&gt;  Bacillus licheniformis

&lt;400&gt;  187

Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala Glu Arg Thr Gly Gly
1               5                   10                  15

Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg Thr Gly Lys Ser Thr
            20                  25                  30

Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu Pro Asn Ile Asn Asn
        35                  40                  45
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Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu Pro Gln Ser Ala Ala
50 55 60

Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe Val Pro Asn Gln Ala
65 70 75 80

Met Ser Val His Val Ser Asp Gly Leu Asp Val Asn Ile Arg Leu Val
85 90 95

Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys Gly Tyr Glu Asp Glu
100 105 110

Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr Glu Glu Pro Ile Pro
115 120 125

Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys Val Ile Gln Glu His
130 135 140

Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly Thr Ile Gly Glu Ile
145 150 155 160

Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg Val Ile Asp Glu Leu
165 170 175

Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile Asn Ser Val Arg Pro
180 185 190

Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu Leu Met Glu Lys Tyr
195 200 205

Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser Met Arg Glu Ala Asp
210 215 220

Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu Phe Pro Val Leu Glu
225 230 235 240

Val Asn Val Asn Leu Pro Ser Trp Val Met Val Leu Lys Glu Asn His
245 250 255

Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys Glu Thr Val Lys Asp
260 265 270

Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val Gly His Phe Ser Glu
275 280 285

Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly Ile Glu Met Gly Gln
290 295 300

Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp Tyr Leu Tyr Asp Glu
305 310 315 320

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Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg Gly Lys Asp His Leu
                325                 330                 335

Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys Thr Glu Tyr Asp Gln
            340                 345                 350

Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr Gly Tyr Gly Ile Ala
        355                 360                 365

Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu Pro Glu Ile Ile Arg
    370                 375                 380

Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala Val Ala Pro Ser Ile
385                 390                 395                 400

His Met Ile Lys Val Asp Val Glu Ser Glu Phe Ala Pro Ile Ile Gly
                405                 410                 415

Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr Leu Met Gln Asp Phe
            420                 425                 430

Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp Ile Phe Gly Arg Ser
        435                 440                 445

Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met
    450                 455                 460

Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr Leu Glu Arg Ile Ile
465                 470                 475                 480

Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile Leu
                485                 490

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<211>  5482
<212>  DNA
<213>  Bacillus licheniformis


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<222>  (501)..(4982)

<400>  188
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ccatgaagag cctgacgctt caagtcgatc cgaataattt cctttactgg attcagatcg     120

gacgcggcgc caataaagaa gcgcttgaga cggcccgtaa gctggaaaac aatgcacaga     180

tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg     240

atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattg aagcggacag     300

cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg     360
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cggacgtaga ggccgcaaag gctgaaacgg agaaggccga gaaggaacag gcgaaaaaag 420

aaaataaaga aaaggaagac aaaaagaaaa aagatgacaa ataaaagcga aaacacctgt 480

tgttggcagg aggcggagaa atg agt ctg tta tgg att ttt tat cat aaa aac 533
Met Ser Leu Leu Trp Ile Phe Tyr His Lys Asn
1 5 10

tat caa aaa ata aaa ctg gat gat cag aac agc cgc acg ctc acc atc 581
Tyr Gln Lys Ile Lys Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile
15 20 25

ggg ccg gat ttg aaa cat tct gtc acg att aag cat ttt tca ttt gaa 629
Gly Pro Asp Leu Lys His Ser Val Thr Ile Lys His Phe Ser Phe Glu
30 35 40

aaa ggc ccg gtg aca ctg gaa aag cag aag gac tca gac gct ttg aac 677
Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn
45 50 55

gtg cag ctg gga ggg gag acg gtc tct tct tta aag ctt ggc gga aag 725
Val Gln Leu Gly Gly Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys
60 65 70 75

gcg tcc gtc caa agc ggc gct gaa cag ctg acg ctc ttt tta gcc gaa 773
Ala Ser Val Gln Ser Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu
80 85 90

gaa gcc gac agc gtt cct gcc tac tat ttg gga gag aga cag gaa atc 821
Glu Ala Asp Ser Val Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile
95 100 105

gtc att tct tcc ctc gat caa gaa gcg gat gtt tat ttc aat gaa acg 869
Val Ile Ser Ser Leu Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr
110 115 120

gat tca ttc ttt gga gaa aaa ggt acg ttc tct ttc atc cgc ctc gac 917
Asp Ser Phe Phe Gly Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp
125 130 135

ggg caa tgg aat gtc ctg ccg aat gac gcg aaa att tat ttg aac gga 965
Gly Gln Trp Asn Val Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly
140 145 150 155

gaa gaa gtg tcc gcc cct gtc tcc gtg caa aat gga gac gaa atc gca 1013
Glu Glu Val Ser Ala Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala
160 165 170

ttt gga ctg aat att ctt cgc atc gtt gaa gac gac ctc ttg gaa atc 1061
Phe Gly Leu Asn Ile Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile
175 180 185

gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg 1109
Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro
190 195 200

agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga 1157
Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg
205 210 215

atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca 1205
Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala
220 225 230 235

cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct 1253
Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro
240 245 250

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ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg      1301
Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro
            255                 260                 265

cgg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg      1349
Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu
        270                 275                 280

att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa      1397
Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys
    285                 290                 295

aga gaa gaa aaa aga gag cgg gtc tat acc ctt tac ctt gaa aac aaa      1445
Arg Glu Glu Lys Arg Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys
300                 305                 310                 315

aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat      1493
Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp
                320                 325                 330

ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc      1541
Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile
            335                 340                 345

agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa      1589
Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln
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atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg      1637
Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu
    365                 370                 375

aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa      1685
Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln
380                 385                 390                 395

acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc      1733
Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile
                400                 405                 410

act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc      1781
Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser
            415                 420                 425

gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc      1829
Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe
        430                 435                 440

cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag      1877
His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu
    445                 450                 455

tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct      1925
Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro
460                 465                 470                 475

cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag      1973
His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln
                480                 485                 490

ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa      2021
Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu
            495                 500                 505

aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca      2069
Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr
        510                 515                 520
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aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc 2117
Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly
525 530 535

aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa 2165
Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys
540 545 550 555

gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa 2213
Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu
560 565 570

cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg 2261
Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro
575 580 585

ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc cgg 2309
Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg
590 595 600

acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct 2357
Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro
605 610 615

gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac 2405
Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp
620 625 630 635

atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg 2453
Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu
640 645 650

gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac 2501
Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn
655 660 665

ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc 2549
Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr
670 675 680

ggt tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca 2597
Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala
685 690 695

gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa 2645
Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys
700 705 710 715

ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga 2693
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720 725 730

acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt 2741
Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu
735 740 745

gcg tcc att aag agc gag ctg aag aaa agg cag cgg ctc ttt gat cag 2789
Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln
750 755 760

tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa 2837
Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys
765 770 775

aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt 2885
Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe
780 785 790 795

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gcc gag ctg aaa agc gaa gaa ccg gaa ttt atc cgc gag ctt gtc agt       2933
Ala Glu Leu Lys Ser Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser
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gcg gca agg atc ggg cga agc ctc ggg gtg cac tta atc ttg gcg acg       2981
Ala Ala Arg Ile Gly Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr
            815                 820                 825

caa aaa ccg ggc ggc atc atc gat gac cag att tgg agc aac tcc aga       3029
Gln Lys Pro Gly Gly Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg
        830                 835                 840

ttc aag gtc gcc ttg aag gtg cag gat gcg aat gac agt aaa gag atc       3077
Phe Lys Val Ala Leu Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile
    845                 850                 855

ctc aaa aac ggg gat gcg gct acc atc acg gta acg ggc cgc ggc tat       3125
Leu Lys Asn Gly Asp Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr
860                 865                 870                 875

ttg caa gtc ggc aac aac gag gtg tat gaa ctg ttc cag tct gca tgg       3173
Leu Gln Val Gly Asn Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp
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agc gga gcc cct tac atg gag gac ggc tac ggc aca gag gat gaa gtg       3221
Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val
            895                 900                 905

gcg atc gtc aca gat acc gga tta att cct tta tca gat gtt gat gct       3269
Ala Ile Val Thr Asp Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala
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gat cgc gct gcg aaa aaa gag gct gtg acg gaa att tcg gca gtc gtc       3317
Asp Arg Ala Ala Lys Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val
    925                 930                 935

gaa caa att gaa cgg att caa gcg gag atg gga atc gag aag ctc ccg       3365
Glu Gln Ile Glu Arg Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro
940                 945                 950                 955

agc cct tgg ctg ccg ccg ctt gaa gaa cgc ata ccg aaa acg cgc tat       3413
Ser Pro Trp Leu Pro Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr
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ccg tcg gag gaa gcc gat gcc ttt aac ttt gcc tat atc gat gaa cct       3461
Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro
            975                 980                 985

gaa aag caa agc cag gag ccg atc agc tac cgc atg atg  gaa gac ggc      3509
Glu Lys Gln Ser Gln Glu Pro Ile Ser Tyr Arg Met Met  Glu Asp Gly
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aat atc  ggc atc gtc ggc tcg  tca ggc tac gga aaa  tcc ctg aca       3554
Asn Ile  Gly Ile Val Gly Ser  Ser Gly Tyr Gly Lys  Ser Leu Thr
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gcc acg  acg ttc atg atg agc  ttt gcc gaa cag tat  acg ccg gaa       3599
Ala Thr  Thr Phe Met Met Ser  Phe Ala Glu Gln Tyr  Thr Pro Glu
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gaa ttg  cat tac tac att ttc  gac ttt ggc aac gga  acg ctg ctt       3644
Glu Leu  His Tyr Tyr Ile Phe  Asp Phe Gly Asn Gly  Thr Leu Leu
    1035                 1040                 1045

ccg ctt  gca agg ctt ccg cac  acc gcg gat tat ttc  ctg atg gac       3689
Pro Leu  Ala Arg Leu Pro His  Thr Ala Asp Tyr Phe  Leu Met Asp
    1050                 1055                 1060
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caa acg aga aaa atc gag aaa ttt atg gtc cgg atc aag gcg gaa 3734
Gln Thr Arg Lys Ile Glu Lys Phe Met Val Arg Ile Lys Ala Glu
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atc gag cac agg aaa aat ctc ttc cgt gca aaa gaa atc agc cat 3779
Ile Glu His Arg Lys Asn Leu Phe Arg Ala Lys Glu Ile Ser His
1080 1085 1090

atc aag atg tac aat gcg ctg aat gag gaa aag ctg ccg ttt att 3824
Ile Lys Met Tyr Asn Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile
1095 1100 1105

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Leu Gly Ile Tyr Leu Ile Leu Thr Ala Thr Arg Val Asn Ala Ile
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gat atc gag ctg ttt gaa ggg atc aaa gcc gac att cag gcg atc 4184
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gca gaa cgc tcg gaa ggc atg aga aag ccg gcg cct gtg ccg atg 4229
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act gtc gaa ccc gta tac ttt aat ctt gag aaa aat aag cac tgc 4364
Thr Val Glu Pro Val Tyr Phe Asn Leu Glu Lys Asn Lys His Cys
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ctc att atg ggt cag acg cag cgc gga aaa aca aac gtc atc aag 4409
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gat caa atc agc tat cta gaa aca aaa gac gac att ctg ctc tgg        4544
Asp Gln Ile Ser Tyr Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp
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ctc gct gag acg gaa gaa att tgc cgg aca agg gaa gcg atg tat        4589
Leu Ala Glu Thr Glu Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr
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ttg gaa gcc gtt aaa caa gga gaa atc gcc aac ctt gat ttc tca        4634
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ccg atg gtc ttt att gtc gac gga att tca cgg ttc cag cag acg        4679
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Ile Asp Ala Ser Ile Gln Asp Lys Met Ala Met Phe Met Lys Ser
    1395                1400                1405

tac gcc cat tta ggt ttc cac ttt ata cct gcc gga aat cac agc        4769
Tyr Ala His Leu Gly Phe His Phe Ile Pro Ala Gly Asn His Ser
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Glu Phe Thr Lys Gly Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln
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gtc aga cac gcg atg cta ttg atg aaa aaa tcc gag cag aac ttg        4859
Val Arg His Ala Met Leu Leu Met Lys Lys Ser Glu Gln Asn Leu
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att cag ctc cca tat gaa cgc cag gag ccg gaa att ctg ccg ggc        4904
Ile Gln Leu Pro Tyr Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly
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Phe Gly Tyr Ile Val Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile
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cct tta tgt gct gta gaa agg aag aaa gcg aaa tgacggaaca             4992
Pro Leu Cys Ala Val Glu Arg Lys Lys Ala Lys
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His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
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Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
50 55 60

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
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Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
85 90 95

Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
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Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
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Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
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Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala
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Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
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Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
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Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
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Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
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Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
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Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
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Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
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Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
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Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
325 330 335

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Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
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Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
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Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
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Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu
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Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
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Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
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Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
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Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
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Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
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Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
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Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
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625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
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660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
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Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
690 695 700

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Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
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Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
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Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val
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770 775 780

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2003/087148 A3

(54) Title: BACILLUS LICHENIFORMIS MUTANT HOST CELL

(57) Abstract: A *Bacillus licheniformis* mutant host cell comprising a mutation (deletion) in one or more genes encoding polypeptides involved in sporulation wherein the mutant host cell expresses at least 5% less of the one or more polypeptides involved in sporulation than the parent host cell, when cultivated under comparable conditions. The mutant host cell is used for producing heterologous polypeptides.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/DK 03/00200

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/75 C12N1/21 C07K14/32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED
Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 03185 A (NOVONORDISK AS ;PRIEST FERGUS G (GB); FLEMING ALASTAIR B (GB); TAN) 30 January 1997 (1997-01-30) the whole document ---	1-21
X	FLEMING A B ET AL: "Extracellular enzyme synthesis in a sporulation-deficient strain of Bacillus licheniformis." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 61, no. 11, November 1995 (1995-11), pages 3775-3780, XP002902964 ISSN: 0099-2240 abstract ---	1-21
X	WO 98 22598 A (NOVO NORDISK BIOTECH INC) 28 May 1998 (1998-05-28) page 6, line 8 - line 11; claims 1,2,17 ---	1-21
	-/--	

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 July 2003	28. 10. 2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Ida Christensen

INTERNATIONAL SEARCH REPORT

Interr al Application No
PCT/DK 03/00200

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
A	WO 02 00907 A (JOERGENSEN STEEN TROELS ;OLSEN CARSTEN (DK); NOVOZYMES AS (DK); AN) 3 January 2002 (2002-01-03) claims -----	6,7

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 03/00200

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-21 (partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1 : claims 1-21 (partially).

A Bacillus licheniformis mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 2.

Invention 2 : claims 1-21 (partially).

A Bacillus licheniformis mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 4.

Invention 3: claims 1-21 (partially).

A Bacillus licheniformis mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 6

Invention 4 : claims 1-21 (partially).

A Bacillus licheniformis mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: ......

etc....
etc....
etc....

Invention 96 :claims 1-21 (partially).

A Bacillus licheniformis mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 191.

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Information on patent family members

International Application No
PCT/DK 03/00200

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